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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03 ; Search time 132.37 Seconds
(without alignments)
6266.684 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactccactgc.....ttctgtgtagtgcacct 385

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:**

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq**
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq**
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq**
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq**
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq**
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq**
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq**
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq**
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq**
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq**
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	7	US-11-344-932-67 Sequence 67, Appl
2	385	100.0	385	10	US-11-349-541-67 Sequence 67, Appl
3	307.2	79.8	3228	7	US-11-344-932-701 Sequence 701, Appl
C 4	231.8	60.2	1016	8	US-11-266-748A-350613 Sequence 350613,
C 5	231.8	60.2	1016	8	US-11-266-748A-383047 Sequence 383047,
6	231.8	60.2	1016	8	US-11-266-748A-433992 Sequence 433992,
7	107.4	27.9	2841	7	US-11-344-932-700 Sequence 700, Appl
8	95	24.7	1016	8	US-11-266-748A-350613 Sequence 350613,
9	95	24.7	1016	8	US-11-266-748A-383047 Sequence 383047,
C 10	95	24.7	1016	8	US-11-266-748A-433992 Sequence 433992,
11	89.2	23.2	5449	8	US-11-266-748A-32477 Sequence 32477, A
C 12	84	21.8	385	7	US-11-344-932-67 Sequence 67, Appl
C 13	84	21.8	385	10	US-11-349-541-67 Sequence 67, Appl
C 14	77.2	20.1	25694	6	US-10-669-920-46 Sequence 46, Appl
C 15	75.2	19.5	154394	8	US-11-266-748A-58517 Sequence 58517, A
16	73.8	19.2	80988	6	US-10-669-920-261 Sequence 261, Appl
C 17	73.8	19.2	421987	8	US-11-266-748A-28210 Sequence 28210, A
C 18	70.4	18.3	3228	7	US-11-344-932-701 Sequence 701, Appl
C 19	69.6	18.1	593	8	US-11-266-748A-254460 Sequence 254460,
20	69.6	18.1	593	8	US-11-266-748A-314977 Sequence 314977,
21	67.6	17.6	198285	8	US-11-266-748A-59857 Sequence 59857, A
C 22	67.6	17.6	4647455	6	US-10-641-321-205 Sequence 205, Appl

23	64.2	16.7	219955	7	US-11-371-354-11185 Sequence 11185, A
24	63.8	16.6	755217	8	US-11-266-748A-29045 Sequence 29045, A
C 25	62.6	16.3	1000	8	US-11-266-748A-200795 Sequence 200795, A
C 26	62.6	16.3	1550	7	US-11-371-354-11257 Sequence 11257, A
C 27	62.6	16.3	1550	7	US-11-266-748A-57638 Sequence 57638, A
C 28	60	15.6	2841	7	US-11-344-932-700 Sequence 700, Appl
C 29	59.2	15.4	1237661	8	US-11-266-748A-29041 Sequence 29041, A
C 30	59	15.3	1071650	8	US-11-266-748A-22664 Sequence 22664, A
31	58.8	15.3	166949	8	US-11-266-748A-60144 Sequence 60144, A
32	53.2	13.8	1000	8	US-11-266-748A-196189 Sequence 196189, A
33	53	13.8	327636	10	US-11-073-360-1613 Sequence 1613, Ap
34	52	13.5	96618	8	US-11-266-748A-24171 Sequence 24171, A
35	51.6	13.4	1237661	8	US-11-266-748A-29041 Sequence 29041, A
36	50.2	13.0	1550	7	US-11-371-354-11257 Sequence 11257, A
37	50.2	13.0	1550	8	US-11-266-748A-57638 Sequence 57638, A
38	49.8	12.9	421987	8	US-11-266-748A-28210 Sequence 28210, A
39	49.4	12.8	420555	6	US-10-669-920-1140 Sequence 1140, Ap
40	49.4	12.8	420555	6	US-11-266-748A-203066 Sequence 203066, A
41	48.4	12.6	1000	8	US-11-266-748A-32477 Sequence 32477, A
C 42	48	12.5	2051	7	US-11-344-932-699 Sequence 699, App
C 43	48	12.5	5449	8	US-11-266-748A-32477 Sequence 32477, A
44	47.4	12.3	31670	10	US-11-330-648-22 Sequence 22, Appl
45	47.4	12.3	31704	6	US-10-669-920-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-11-344-932-67
; Sequence 67, Application US/11344932
; Publication NO. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Fa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-67

Query Match      100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATTCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATTCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTTCATTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTTCATTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Db 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2
US-11-349-541-67
; Sequence 67, Application US/11349541
; Publication No. US20060223129A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-349-541-67

Query Match      100.0%; Score 385; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATTCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATTCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTTCATTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTTCATTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Db 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3
US-11-344-932-701
; Sequence 701, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C32
;; CURRENT APPLICATION NUMBER: US/11/344,932
;; CURRENT FILING DATE: 2006-02-01
;; PRIOR APPLICATION NUMBER: 10/144,678
;; PRIOR FILING DATE: 2002-05-09
;; PRIOR APPLICATION NUMBER: 10/012,896
;; PRIOR FILING DATE: 2001-12-10
;; PRIOR APPLICATION NUMBER: 09/895,814
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: 09/852,911
;; PRIOR FILING DATE: 2001-05-09
;; PRIOR APPLICATION NUMBER: 09/780,669
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 09/759,143
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: 09/709,729
;; PRIOR FILING DATE: 2000-11-09
;; PRIOR APPLICATION NUMBER: 09/685,166
;; PRIOR FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: 09/679,426
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 09/657,279
;; PRIOR FILING DATE: 2000-09-06
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1033
;; SOFTWARE: Fast-SEQ for Windows Version 3.0
;; SEQ ID NO 701
;; LENGTH: 3228
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 66, 2343, 2387, 3065
;; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-701

Query Match 79.8%; Score 307.2; DB 7; Length 3228;
Best Local Similarity 92.0%; Pred. No. 1.4e-92;
Matches 346; Conservative 0; Mismatches 28; Indels 2; Gaps 2;
QY 12 TCACCTTGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGAGGTCGGACCA 71
Db 292 TCCACTTGCCCTTGTGAGACACTTTATCCAGCACTTTAGGAATGCTGAGGTCATACCA 351
QY 72 CCACATCTCATGTCAGAGATGCCCCAGCAGACATCAGGTCGAGAGTCCCTTTT-AA 130
Db 352 CCACATCTTATATGCAAGATGCCCCAGCAGATCAGGTCGGAGAGTCCCTTTTAA 411
QY 131 AAAGGGGACTTGCTTAA-AAAGAGTCTAGCCACGATTTGTGTAGAGCAGCTGTGTG 189
Db 412 AAAGGAGACTTGCTTAAATAAGAGTCTAGCCACGTTTGTGTAGAGCGCTGTGTG 471
QY 190 CTGAGATTCACATTTTGTGAGAGTCTCTCTCTGAGACCTGATCTTTAGAGGCTGGCAGT 249
Db 472 CTGGGGTTCACATTTTGTGAGAGTCTCTCTCTGAGACCTGATCTCTGGAGGCTGGGCA 531
QY 250 CTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGTGCTCTCTCCCA 309
Db 532 CTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGTGCTCTCTCCCA 591
QY 310 GGCCCCCAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATACCATAGTTTC 369
Db 592 TGGCCCCAGCTGGCCACACCTGCTTACGGGGCAGCTCTTAGATGCCACACCATAGTTTC 651
QY 370 TGTGCTAGTGGACCGT 385
Db 652 CATGCTAGTGGACTGT 667

RESULT 4
US-11-266-748A-350613/c
; Sequence 350613, Application US/11266748A

;; Publication No. US20060134663A1
;; GENERAL INFORMATION:
;; APPLICANT: Harkin, Paul
;; APPLICANT: Johnston, Patrick
;; APPLICANT: Mulligan, Karl
;; TITLE OF INVENTION: Transcriptome Microarray Technology and
;; TITLE OF INVENTION: Methods of Using the Same
;; FILE REFERENCE: 55815-0102 (319189)
;; CURRENT APPLICATION NUMBER: US/11/266,748A
;; CURRENT FILING DATE: 2005-11-03
;; PRIOR APPLICATION NUMBER: EP 04105479.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105482.6
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105483.4
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105507.0
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105485.9
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105484.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: US 60/662,276
;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700,293
;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 350613
;; LENGTH: 1016
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (880)..(881)
;; OTHER INFORMATION: n is a, c, g, or t
;; NAME/KEY: misc feature
;; LOCATION: (964)..(972)
;; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-350613

Query Match 60.2%; Score 231.8; DB 8; Length 1016;
Best Local Similarity 88.0%; Pred. No. 1.9e-67;
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;
QY 11 CTCACCTGCGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGAGTCCGACCA 70
Db 442 CTCACGCTGCTTGTGAGATCTTTATCCAGCACTTTAGGAATGCTAAAGTTCAGATCA 383
QY 71 GCCACATCTCATGTCAGAGATTTGCCAGCAGATCAGCTGTAGAGCTGCTGTGTC 130
Db 382 GCCCATCTCATGTTCAAGACTGCCCCAGCAGAGATCAGTCCAGAGTTCCTCTTCAA 323
QY 131 AAAGGGGACTTCTCTTAAAGAAAGTCTAGCCACGATTTGTGTAGAGCAGCTGTGCTGTC 190
Db 322 AAAGGGGACTTCTCTTAAAGAAAGTCTAGCCATGTTGTGTAAAGCAGCTGTGCTGTC 263
QY 191 TGGAGATTCACATTTTGTGAGAGATTTCTCTCTGAGACCTGATCTTTAGAGCTGGGCA 250
Db 262 CGGGGGTTCACATTTTGTGAGACAGTCTCTCTCTGAGACCTGATCTCT- ---GCTGGG 207
QY 251 TTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTCTAGTCTGCTGCTCTCCCA 310
Db 206 CTGACATGAGATGGGGCTGGTCTGATCTATATCAGCACTCCCTAGTCTGCTGCTCTCCCA 147
QY 311 G 311
Db 146 G 146

RESULT 5
US-11-266-748A-383047/c

; Sequence 383047, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 383047
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (880)..(881)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (964)..(972)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-383047

Query Match 60.2%; Score 231.8; DB 8; Length 1016;
Best Local Similarity 88.0%; Pred. No. 1.9e-67;
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;
Qy 11 CTCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTCCTCTTTAA 70
Db 442 CTCACGTGCTTGTGAGATCTTTATCCAGCCTTTAGGAATGCTAAGTTCAGATCA 383
Qy 71 GCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTCCTCTTTAA 130
Db 382 GCCCATCTCATGTTCAGACTGCCAGCAGAGATCAGTTCACAGATTCCTCTTCAA 323
Qy 131 AAAGGGGACTTGTCTTAAAGAGCTTAGCCACAGTGTGTAGAGCAGCTGTGCTGTC 190
Db 322 AAAGGGGACTTGTCTTAAAGAGCTTAGCCATGTTGTGTAAAGCAGCTATGCTGTC 263
Qy 191 TGGAGATTTCATTTTGTAGAGAGTCTCTCTGAGACCTGATCTTTTAGAGGCTGGCAGTC 250
Db 262 CGGGGGTTCATTTTGTAGACAGTCTCTCTGAGACCTGATCTCT- - - - -GCTGGGCGATC 207
Qy 251 TTGCACATGAGATGGGGCTGGTCTGATCTCAGACTCTCTTAGTCTGCTTGCCTCTCCAG 310
Db 206 CTGCACATGAGATGGGGCTGGTCTGATATCAGACTCTCCCTAGTCTGCTTGCCTCTCCAG 147
Qy 311 G 311
Db 146 G 146

RESULT 6

US-11-266-748A-433992
; Sequence 433992, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 433992
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)..(53)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(137)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-433992

Query Match 60.2%; Score 231.8; DB 8; Length 1016;
Best Local Similarity 88.0%; Pred. No. 1.9e-67;
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;
Qy 11 CTCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTCCTCTTTAA 70
Db 575 CTCACGTGCTTGTGAGATCTTTATCCAGCCTTTAGGAATGCTAAGTTCAGATCA 634
Qy 71 GCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTCCTCTTTAA 130
Db 635 GCCCATCTCATGTTCAGACTGCCAGCAGAGATCAGTTCACAGATTCCTCTTCAA 694
Qy 131 AAAGGGGACTTGTCTTAAAGAGCTTAGCCACAGTGTGTAGAGCAGCTGTGCTGTC 190
Db 695 AAAGGGGACTTGTCTTAAAGAGCTTAGCCATGTTGTGTAAAGCAGCTATGCTGTC 754
Qy 191 TGGAGATTTCATTTTGTAGAGAGTCTCTCTGAGACCTGATCTTTTAGAGGCTGGCAGTC 250
Db 755 CGGGGGTTCATTTTGTAGACAGTCTCTCTGAGACCTGATCTCT- - - - -GCTGGGCGATC 810
Qy 251 TTGCACATGAGATGGGGCTGGTCTGATCTCAGACTCTCTTAGTCTGCTTGCCTCTCCAG 310
Db 811 CTGCACATGAGATGGGGCTGGTCTGATATCAGACTCTCCCTAGTCTGCTTGCCTCTCCAG 870
Qy 311 G 311
Db 871 G 871

RESULT 7

US-11-344-932-700
; Sequence 700, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C32

; CURRENT APPLICATION NUMBER: US/11/344,932

; CURRENT FILING DATE: 2006-02-01

; PRIOR APPLICATION NUMBER: 10/144,678

; PRIOR FILING DATE: 2002-05-09

; PRIOR APPLICATION NUMBER: 10/012,896

; PRIOR FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 09/895,814

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 09/852,911

; PRIOR FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: 09/780,669

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 09/759,143

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/709,729

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 09/685,166

; PRIOR FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: 09/679,426

; PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: 09/657,279

; PRIOR FILING DATE: 2000-09-06

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 700

; LENGTH: 2841

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1447, 2244

; OTHER INFORMATION: n = A,T,C or G

US-11-344-932-700

Query Match

Best Local Similarity 27.9%; Score 107.4; DB 7; Length 2841;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

277 TCTCAGCACTCCTTAGTCTGCTTCCAGGGGCCAGCCTGGCCACACCTGCTTA 336

Db 1304 TCCAGCACTCCTTAGTCTGCTTCCAGGGGCCAGCCTGGCCACACCTGCTTA 1363
QY 337 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT 385
Db 1364 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT 1412

RESULT 8

US-11-266-748A-350613
; Sequence 350613, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/562,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 350613

; LENGTH: 1016

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (880)..(881)

; OTHER INFORMATION: n is a, c, g, or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (964)..(972)

; OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-350613

Query Match 24.7%; Score 95; DB 8; Length 1016;

Best Local Similarity 65.1%; Pred. No. 2.2e-21;

Matches 157; Conservative 0; Mismatches 80; Indels 4; Gaps 1;

QY 51 GGAATGCTGAGTGGACAGCCACATCTCATGTCGAAGATTGCCAGCAGACATCAGGT 110

Db 169 GGAGTGTGATATCAGACCCCATCTCATGTGTCAGGACTGCCAGCAGAGATCAGGT 228

QY 111 CTGAGAGTTCCCTTTTAAAGGGGACTTGTCTTAAAAAGAACTGTAGCCACGATTGT 170

Db 229 CTCAGAGGAGAACTGTCTCAAAAGTGAACCCCGGCACAGCATAGCTGCTTTACAAAC 288

QY 171 GTAGAGCAGCTGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCTCTGAGACCTGA 230

Db 289 ATGGCCAGGCTTCTTTTGGAGAACTCCCTTTTGAAGAGGGGAACTCTGGGAACCTGA 348

QY 231 TCTTTAGAGGCTGGCAGTCTTGTGACATGAGATGGGCTGTCTGATCTCAGCATCTCTT 290

Db 349 TCTCT---GCTGGCAGTCTTTGAACATGAGATGGGCTGTGATCTGAACTTAGCATTTCTTA 404

US-11-266-748A-32477
; Sequence 32477, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32477
; LENGTH: 5449
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-32477

Query Match 23.2%; Score 89.2; DB 8; Length 5449;
Best Local Similarity 79.1%; Pred. No. 5e-19;
Matches 106; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 252 TGCACATGATGGGCTGGTCTGATCTCAGCACTCTTGTGCTTCCCTCTCCAGG 311
Db 3931 TCCACTTGCCTTGTGAGACACTTTGTCCACACTCTTGTGCTTCCCTCTCCAGT 3990
QY 312 GCCCAGCTGCCACCTGCTTACAGGGCACTCTCAGATGCCATACATAGTTCTG 371
Db 3991 GCCCAGCTGGCCACACTGCTTACGGGGCACTCTTATAGTCCCAACACATAGTTCCA 4050
QY 372 TGCTAGTGGACCGT 385
Db 4051 TGCTAGTGGACTGT 4064

RESULT 12
US-11-344-932-67/c
; Sequence 67, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-67

Query Match 21.8%; Score 84; DB 7; Length 385;
Best Local Similarity 64.5%; Pred. No. 6.7e-18;
Matches 160; Conservative 0; Mismatches 80; Indels 8; Gaps 2;
QY 48 TTAGGATGCTGAGTCGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGC---AGAC 103
Db 291 TAAGGATGCTGAGATCAGACCGCCCATCTCATGTGCAAGACTGCCAGCCTCTAAG 232
QY 104 ATCAGGCTGAGAGTTCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGAGTCTAGCCA 163
Db 231 ATCAGGCTCAGAGGAGAACTCTCTCAAAGTGAATCTCCAGCACAGCACAGCTGCTCTA 172
QY 164 CGATTGCTGAGAGAGCTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGA 223
Db 171 CACAATCGTGGCTAGACTTCTTTTAAAGCAAGTCCCTCTTTTAAAAAGGGAAGTCTCA 112
QY 224 GACCTGATCTTTAGAGGCTGGGAGCTTTGACATGAGATGGGGCTGCTGATCTCAGC 283
Db 111 GACCTGATGCTCT---GCTGGCAATCTTGACATGAGATGGGCTGCTCGACCTCAGC 56
QY 284 ACTCCTTA 291
Db 55 ATTCTTAA 48

RESULT 13
US-11-349-541-67/c
; Sequence 67, Application US/11349541
; Publication No. US20060223129A1

Db 25091 GCAGGGTGTCTTTGCCCATGAGACAGGACTAGTCTGATCTGAGCACCCCTTAGTCTGATG 25032
QY 300 GCCTCTCCCAAGGGCCCCCAGCGCTGGCCACACCTGCTTACAGGGCA 343
Db 25031 GCCTCTCTGAGGGCCCCAGCGCTGGCCACAACTGCTTGCAGTGCA 24988

Search completed: December 31, 2006, 19:49:14
Job time : 139.37 secs

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Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGCTTCTCTGTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGCTTCTCTGTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTCCTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2

US-09-780-669-67
; Sequence 67, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGCTTCTCTGTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGCTTCTCTGTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTCCTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3

US-09-030-606-67
; Sequence 67, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACTACACACACTCCACTTGGCCCTTGTGAGACACATTTGTCCAGCACCTTTAGGAATCCTGA	60
Db	1	ACTACACACACTCCACTTGGCCCTTGTGAGACACATTTGTCCAGCACCTTTAGGAATCCTGA	60
Qy	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCCTCAGAGTTC	120
Db	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCCTCAGAGTTC	120
Qy	121	CCCTTTTAAAAAAGGGGACTTGCCTTTAAAAAAGAAAGTCTTAGCCACGATTGTTGATAGACAGC	180
Db	121	CCCTTTTAAAAAAGGGGACTTGCCTTTAAAAAAGAAAGTCTTAGCCACGATTGTTGATAGACAGC	180
Qy	181	TGTGCTGTGCTCGAGATTCACTTTTGTGAGAGAGTTCCTCCTGTGAGACCTGATCTCTTTAGAGG	240
Db	181	TGTGCTGTGCTCGAGATTCACTTTTGTGAGAGAGTTCCTCCTGTGAGACCTGATCTCTTTAGAGG	240
Qy	241	CTGGGCAAGCTTTGCACATGAGATGGGCTGCTCGATCTCAGCACCTCTTAGTCTCTCTTG	300
Db	241	CTGGGCAAGCTTTGCACATGAGATGGGCTGCTCGATCTCAGCACCTCTTAGTCTCTCTCTTG	300
Qy	301	CCTCTCCACAGGCCCCAGCCTGGCCACACCTGCTTTACAGGCACTCTTCAGATGCCCATAC	360
Db	301	CCTCTCCACAGGCCCCAGCCTGGCCACACCTGCTTTACAGGCACTCTTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGACCGT	385

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RESULT 4
US-09-822-827-67
; Sequence 67, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-67

```

Query Match	100.0%	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 2.2e-126;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACTACACACACTCCACTTGCCTTGTGAGACACACTTTGTCCCGACACACTTTAGGAATGCTGA	60	
Db	1	ACTACACACACTCCACTTGCCTTGTGAGACACACTTTGTCCCGACACACTTTAGGAATGCTGA	60	
Qy	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGCACATCAGGTCCTGAGAGTTC	120	
Db	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGCACATCAGGTCCTGAGAGTTC	120	
Qy	121	CCCTTTTAAAAAGGGGACTTGGCTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGACGAGC	180	
Db	121	CCCTTTTAAAAAGGGGACTTGGCTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGACGAGC	180	
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Qy	241	CTGGCGAGTCTTGACATGATGGGCGTGGTCTGATCTCAGCACTCCTTAGTCTCGTTG	300	
Db	241	CTGGCGAGTCTTGACATGATGGGCGTGGTCTGATCTCAGCACTCCTTAGTCTCGTTG	300	
Qy	301	CCTCTCCAGGGCCCCAGCCTGGGCCACACCTGGCTTTACAGGGCACTCTCAGATGCCCATAC	360	

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Db      301   CCTCTCCCGAGGGCCCCACGCTTTCAGATGCCCATC 360
          |||||
QY      361   CATAGTTTCTGTGCTAGTGGAACCGT 385
          |||||
Db      361   CATAGTTTCTGTGCTAGTGGAACCGT 385
          |||||

RESULT 5
US-09-115-453-67
; Sequence 67, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLIEE: Dillion, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
;     TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-67
```

Query Match	100.0.0%;	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0.0%;	Pred. No. 2.2e-126;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTGCCAGACACTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTGCCAGACACTTTAGGAATGCTGA	60
Qy	61	GGTCGGACACAGCCACATCTCATGTGCAAGATTGCCCGACGACACATCAGGTCAGAGTTC	120
Db	61	GGTCGGACACAGCCACATCTCATGTGCAAGATTGCCCGACGACACATCAGGTCAGAGTTC	120
Qy	121	CCCTTTTAAAAAGGGGACCTTGCTTAAAAAGAGTCTAGCCACGATTGTGTACAGCAGC	180
Db	121	CCCTTTTAAAAAGGGGACCTTGCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC	180
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG	240
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG	240
Qy	241	CTGGCAGCTTTCGACATGAGATGGGCTGGTCTGATCTCAGCAGCTCCTTAGTCTGCTTG	300
Db	241	CTGGCAGCTTTCGACATGAGATGGGCTGGTCTGATCTCAGCAGCTCCTTAGTCTGCTTG	300
Qy	301	CCCTCTCCAGGGGCCAGCCTGGCCACACCTGCTTACAGGGGCACCTCTCAGATGCCCATAC	360
Db	301	CCCTCTCCAGGGGCCAGCCTGGCCACACCTGCTTACAGGGGCACCTCTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGTCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTCTAGTGGACCGT	385

RESULT 6
US-09-232-880-67
; Sequence 67, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232.880.

```
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACCTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
Db 1 ACTACACACCTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTGCGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGGCACTTGTGCATGAGATGGGCTGTGCTGATCTCAGACCTCTTAGTCTGCTTG 300
Db 241 CTGGGCACTTGTGCATGAGATGGGCTGTGCTGATCTCAGACCTCTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATPAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATPAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 7
US-09-895-793-67
; Sequence 67, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACCTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
Db 1 ACTACACACCTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTGCGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGGCACTTGTGCATGAGATGGGCTGTGCTGATCTCAGACCTCTTAGTCTGCTTG 300
Db 241 CTGGGCACTTGTGCATGAGATGGGCTGTGCTGATCTCAGACCTCTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATPAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATPAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 8
US-09-895-814-67
; Sequence 67, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
```

FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGAGAGATTCACTTTTTCAGAGAGTTTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGATTCACTTTTTCAGAGAGTTTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGCTTGGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
DB 241 CTGGGCGAGCTTGGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTGTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTGTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTCTGTGCTAGTGGACCGT 385

RESULT 9
US-10-012-896-67
Sequence 67, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-67

Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGAGAGATTCACTTTTTCAGAGAGTTTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGATTCACTTTTTCAGAGAGTTTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGCTTGGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
DB 241 CTGGGCGAGCTTGGACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTGTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTGTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTCTGTGCTAGTGGACCGT 385

RESULT 10
US-10-010-940-67
Sequence 67, Application US/10010940
Publication No. US2003008062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapien
US-10-010-940-67

Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTCTGGAGATTCACCTTTTGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTCTGGAGATTCACCTTTTGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGCAGCTTTGCACATGAGATGGGCTGTGTGATCTGATCTCAGACCTCTTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGCACATGAGATGGGCTGTGTGATCTCAGACCTCTTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 11

US-10-144-678A-67

; Sequence 67, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-144-678A-67

Query Match 100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTCTGGAGATTCACCTTTTGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTCTGGAGATTCACCTTTTGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGCAGCTTTGCACATGAGATGGGCTGTGTGATCTCAGACCTCTTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGCACATGAGATGGGCTGTGTGATCTCAGACCTCTTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 12

US-10-294-025-67

; Sequence 67, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-294-025-67

Query Match 100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTCTGGAGATTCACCTTTTGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGTGGAGATTCACTTTTGAGAGAGTTCTCTTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGTCTTGACATGAGATGGGCTGCTGTGATCTCAGCACTCTTAGTCTGTTG 300
Db 241 CTGGGAGTCTTGACATGAGATGGGCTGCTGTGATCTCAGCACTCTTAGTCTGTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTCTGTGCTAGTGACCGT 385
Db 361 CATAGTTCTGTGCTAGTGACCGT 385

RESULT 13
US-10-688-838-67
; Sequence 67, Application US/10688838
; Publication No. US20040141989A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D4
; CURRENT APPLICATION NUMBER: US/10/688,838
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-688-838-67

Query Match 100.0%; Score 385; DB 8; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGAGCCAGCCACATCTCATGTCGAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGAGCCAGCCACATCTCATGTCGAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGTTG 300
Db 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTCTGTGCTAGTGACCGT 385
Db 361 CATAGTTCTGTGCTAGTGACCGT 385

RESULT 14
US-11-234-786-67
; Sequence 67, Application US/11234786
; Publication No. US20060024301A1

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-67

Query Match 100.0%; Score 385; DB 16; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGAGCCAGCCACATCTCATGTCGAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGAGCCAGCCACATCTCATGTCGAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGTTG 300

Db 241 CTGGCAGCTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCCAGCCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGCCCCCAGCCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 15

US-10-294-025-1036
; Sequence 1036, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1036
; LENGTH: 3710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-1036

Query Match 99.2%; Score 381.8; DB 7; Length 3710;
Best Local Similarity 99.5%; Pred. No. 8.4e-125;
Matches 383; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
Db 2282 ACCACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 2341
Qy 61 GGTGGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
Db 2342 GGTGAGACCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 2401
Qy 121 CCCTTTAAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 2402 CCCTTTAAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 2461
Qy 181 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240
Db 2462 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 2521
Qy 241 CTGGGCAGTCTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 2522 CTGGGCAGTCTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 2581
Qy 301 CCTCTCCAGGCCCCCAGCCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCATAC 360
Db 2582 CCTCTCCAGGCCCCCAGCCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCATAC 2641
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 2642 CATAGTTTCTGTGCTAGTGGACCGT 2666

Search completed: December 31, 2006, 13:56:03
Job time : 615.045 secs


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Qy 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Db |||||
1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Qy 61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db |||||
61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Db |||||
121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Db |||||
181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db |||||
241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Db |||||
301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
Db |||||
361 CATAGTTTCTGTGCTAGTGAGACCGT 385
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RESULT 2

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US-09-030-607-67
; Sequence 67, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-67
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Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Db |||||
1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Qy 61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db |||||
61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Db |||||
121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Db |||||
181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db |||||
241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Db |||||
301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
Db |||||
361 CATAGTTTCTGTGCTAGTGAGACCGT 385
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RESULT 3

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US-09-439-313-67
; Sequence 67, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-67
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Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Db |||||
1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60
Qy 61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
Db |||||
61 GGTGGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTGAGAGTTC 120
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QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGTAGACCTGTATCTTTAGAGG 240
Db 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGTAGACCTGTATCTTTAGAGG 240
QY 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
Db 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360
QY 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 4

US-09-352-616A-67
; Sequence 67, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTTAGGAATGCTGA 60
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGAGACCTGTATCTTTAGAGG 240
Db 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGAGACCTGTATCTTTAGAGG 240
QY 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
Db 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 5

US-09-232-149A-67
; Sequence 67, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTTAGGAATGCTGA 60
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGAGACCTGTATCTTTAGAGG 240
Db 181 TGTGCTGTGTGGAGATTCATCTTTTGTAGAGAGTTCTCTCTGAGACCTGTATCTTTAGAGG 240
QY 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
Db 241 CTGGGAGTCTTGCACATGAGATGGGCTGGTCTGTATCTCAGCACCTCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGTCTTACAGGGCCTCTCTCAGATGCCATAC 360
QY 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 6

US-09-159-812-67
; Sequence 67, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGAGACCGT 385

RESULT 7
US-09-636-215-67
; Sequence 67, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGAGACCGT 385

RESULT 8
US-09-685-166A-67
; Sequence 67, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
QY 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300
DB 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 9

US-09-115-453-67
; Sequence 67, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
QY 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300
DB 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385
RESULT 10
US-09-688-489-67
; Sequence 67, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTGCTGCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180
QY 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGATTCACTTTTGTGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300
DB 241 CTGGGACAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 11

US-09-679-426-67
; Sequence 67, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCAGACACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCAGACACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCTCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCTCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCTGAGAGTTC 180
Db 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCTGAGAGTTC 180
Qy 181 TGTGCTGTGCGAGATTCACATTTTGAGAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCGAGATTCACATTTTGAGAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGACCGT 385

RESULT 12
US-09-759-143-67
; Sequence 67, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCAGACACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCAGACACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCTCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCTCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCTGAGAGTTC 180
Db 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCTGAGAGTTC 180
Qy 181 TGTGCTGTGCGAGATTCACATTTTGAGAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCGAGATTCACATTTTGAGAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGACCGT 385

RESULT 13
US-09-651-236-67
; Sequence 67, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
US-09-651-236-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGAGAGTTCATTTTTCAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGTTCATTTTTCAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTTGTGCTGCTTG 300
DB 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTTGTGCTGCTTG 300
QY 301 CCTCTCCAGGGCCAGCTGCGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCAGCTGCGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTCTGTGCTAGTGAGCCGT 385
DB 361 CATAGTTCTGTGCTAGTGAGCCGT 385

RESULT 14
US-09-030-606-67
Sequence 67, Application US/09030606
Patent No. 6887660
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GTGCGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GTGCGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGAGAGTTCATTTTTCAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGTTCATTTTTCAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTTGTGCTGCTTG 300
DB 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTTGTGCTGCTTG 300
QY 301 CCTCTCCAGGGCCAGCTGCGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCAGCTGCGCCACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTCTGTGCTAGTGAGCCGT 385
DB 361 CATAGTTCTGTGCTAGTGAGCCGT 385

RESULT 15
US-09-657-279-67
Sequence 67, Application US/09657279
Patent No. 6894146
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C19

; CURRENT APPLICATION NUMBER: US/09/657,279

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 877

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-657-279-67

Query Match 100.0%; Score 385; DB 3; Length 385;

Best Local Similarity 100.0%; Pred. No. 5.9e-124;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

Db 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

Qy 61 GGTCCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

Db 61 GGTCCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

Qy 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180

Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180

Qy 181 TGTGCTGTGCTGGAGATTTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGCTGGAGATTTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGCAGTCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

Db 241 CTGGCAGTCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCAGTCTCAGATGCCCATAC 360

Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCAGTCTCAGATGCCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Search completed: December 31, 2006, 12:31:10

Job time : 90.8616 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 299.256 Seconds
(without alignments)
8969.963 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactccactgtg.....ttctgtgtagggaccgt 385

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_8 :
1: Geneseqn1980s :
2: Geneseqn1990s :
3: Geneseqn2000s :
4: Geneseqn2001as :
5: Geneseqn2001bs :
6: Geneseqn2002as :
7: Geneseqn2002bs :
8: Geneseqn2003as :
9: Geneseqn2003bs :
10: Geneseqn2003cs :
11: Geneseqn2003ds :
12: Geneseqn2004as :
13: Geneseqn2004bs :
14: Geneseqn2005s :
15: Geneseqn2006s :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	100.0	385	2	AAV58544
2	385	100.0	385	2	AAV61287
3	385	100.0	385	3	AAA06307
4	385	100.0	385	3	ABS71212
5	385	100.0	385	4	AAH93423
6	385	100.0	385	4	AAH93423
7	385	100.0	385	4	AAH02488
8	385	100.0	385	4	AAH84737
9	385	100.0	385	4	AAH84737
10	385	100.0	385	5	ACA59324
11	385	100.0	385	5	AAH10066
12	385	100.0	385	6	ABL94887
13	385	100.0	385	6	ABS58596
14	385	100.0	385	8	ACC95051
15	385	100.0	385	10	ADH13517
16	385	100.0	385	10	ADG26933
17	385	100.0	385	15	AEF66214
18	381.8	99.2	3710	10	ADH14486

19	318.2	82.6	1177	11	ACN90108	Acn90108 Breast ca
20	307.2	79.8	3218	15	AEF66848	Aef66848 Human pro
21	307.2	79.8	3228	4	AAH93865	Aah93865 P704P cDN
22	307.2	79.8	3228	4	AAH93865	Aah93865 P704P cDN
23	307.2	79.8	3228	4	AAH93865	Aah93865 P704P cDN
24	307.2	79.8	3228	5	ACA59845	Acas59845 Prostate
25	307.2	79.8	3228	6	ABL95408	AbL95408 Human P70
26	307.2	79.8	3228	8	ACC95572	Acc95572 Prostate
27	307.2	79.8	3228	10	ADG26567	Adg26567 Human pro
28	307.2	79.8	3228	10	ADG26567	Adg26567 Human pro
29	288.2	74.9	620	4	AAH18894	Aah18894 Human bre
30	288.2	74.9	620	4	AAH18894	Aah18894 Human bre
31	259.8	67.5	656	11	ACN87074	Acn87074 Breast ca
32	237.2	61.6	831	5	ABV26126	Abv26126 Human pro
33	237.2	61.6	831	5	ABV26126	Abv26126 Human pro
34	237.2	61.6	831	5	ABV26126	Abv26126 Human pro
35	237.2	61.6	831	5	ABV26126	Abv26126 Human pro
36	224.8	58.4	516	4	AAH14082	Aah14082 Human bre
37	200	51.9	875	11	ACN81332	Acn81332 Breast ca
38	175.4	45.6	383	4	AAH15514	Aah15514 Human bre
39	175.4	45.6	407	4	AAH24358	Aah24358 Human bre
40	175.4	45.6	897	11	ACN85503	Acn85503 Breast ca
41	175.4	45.6	899	11	ACN91316	Acn91316 Breast ca
42	173.8	45.1	435	4	AAH18756	Aah18756 Human bre
43	172	44.7	354	4	AAH20352	Aah20352 Human bre
44	172	44.7	361	4	AAH11453	Aah11453 Human bre
45	172	44.7	417	11	ACN81654	Acn81654 Breast ca

ALIGNMENTS

RESULT 1

AAV58544

ID AAV58544 standard; cDNA; 385 BP.

XX

AC AAV58544;

XX

25-MAR-2003 (revised)

DT 08-DEC-1998 (first entry)

XX

DE Prostate tumour specific gene clone P80.

XX

KW Prostate tumour specific gene; human; prostate cancer; detection;

KW therapy; ss.

XX

OS Homo sapiens.

XX

PN WO9837418-A2.

XX

PD 27-AUG-1998.

XX

PF 25-FEB-1998; 98WO-US003690.

XX

PR 25-FEB-1997; 97US-00806596.

PR

01-AUG-1997; 97US-00904809.

PR

09-FEB-1998; 98US-00020747.

XX

(CORI-) CORIXA CORP.

PI Xu J, Dillon DC;

XX

WPI; 1998-480805/41.

XX

Novel human prostate specific tumour protein and fragments - useful for

detecting and treating prostate cancers.

PS Claim 1; Page 64; 141pp; English.

XX

This sequence represents a human prostate tumour specific gene, and can

be used in the method of the invention. The method is for detecting

prostate cancer comprises contacting a biological sample with an agent

able to bind an immunogenic portion of a prostate protein (such as

CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may also
CC be conjugated to a therapeutic agent for use in therapy of prostate
CC cancers. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ

Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTCAGACATTTGCCAGACATTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTCAGACATTTGCCAGACATTTAGGAATGCTGA 60
Qy 61 GGTGGACACGACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACACGACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGCATTTGTGTGAGAGCAGC 180
Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGCATTTGTGTGAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTTCATTTTGAAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTTCATTTTGAAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGTGATCTCAGCAGCTCCTTGTAGTCTGCTTG 300
Db 241 CTGGCAGTCTTGACATGAGATGGGCTGTGATCTCAGCAGCTCCTTGTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2

AAV61287
ID AAV61287 standard; cDNA; 385 BP.

XX AAV61287;

AC 06-JAN-1999 (first entry)

DT cDNA sequence of prostate tumour clone P80.

DE Prostate; cancer; tumour; vaccine; immunogen; clones; ss.

XX Homo sapiens.

OS WO9837093-A2.

XX 27-AUG-1998.

XX 25-FEB-1998; 98WO-US003492.

XX 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 09-FEB-1998; 98US-00020956.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC;

XX WPI; 1998-609886/51.

XX Polypeptides comprising immunogenic portions of prostate proteins - used

PT in a vaccine for the treatment of prostate cancer.

XX Claim 12; Page 61; 130pp; English.

XX The present sequence is a DNA which encodes an immunogenic portion of a
CC prostate tumour protein. The encoded immunogen, or the DNA itself, can be
CC used as a vaccine for the treatment of prostate cancer. The DNA was
CC identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library

XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 2; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.8e-117;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTCAGACATTTGCCAGACATTTAGGAATGCTGA 60

Db 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTGTCAGACATTTGCCAGACATTTAGGAATGCTGA 60

Qy 61 GGTGGACACGACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120

Db 61 GGTGGACACGACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120

Qy 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGCATTTGTGTGAGAGCAGC 180

Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGCATTTGTGTGAGAGCAGC 180

Qy 181 TGTGCTGTGCTGGAGATTTCATTTTGAAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGCTGGAGATTTCATTTTGAAGAGTCTCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGTGATCTCAGCAGCTCCTTGTAGTCTGCTTG 300

Db 241 CTGGCAGTCTTGACATGAGATGGGCTGTGATCTCAGCAGCTCCTTGTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360

Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3

AAA06307

ID AAA06307 standard; cDNA; 385 BP.

XX AAA06307;

AC 13-JUN-2000 (first entry)

DT Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:67.

DE Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX immunogenic; cytostatic; vaccine; ss.

XX Homo sapiens.

XX WO200004149-A2.

XX 27-JAN-2000.

XX 14-JUL-1999; 99WO-US015838.

XX 14-JUL-1998; 98US-00115453.

PR 14-JUL-1998; 98US-00116134.

PR 23-SEP-1998; 98US-00159612.

PR 23-SEP-1998; 98US-00159622.

PR 15-JAN-1999; 99US-00232149.

PR 15-JAN-1999; 99US-00232880.

PR 09-APR-1999; 99US-00288946.


```
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 50; Page 120; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumor protein (PTP). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express the
XX polypeptides, antibodies against the polypeptides and vaccines comprising
XX them can be used for inhibiting the development of prostate cancer in a
XX patient. The polypeptides can be used to generate antibodies or anti-
XX idiotypic antibodies for passive immuno therapy. A portion of the
XX polynucleotides encoding the polypeptides can be used as a probe or to
XX modulate the expression of the polypeptides. AA06241 to AAA06691 and
XX AA082000 to AA082020 represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 3; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX
XX QY 61 GGTGGGACAGCCAGCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
XX DB 61 GGTGGGACAGCCAGCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
XX
XX QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX
XX QY 181 TGTGCTGTCTGAGAGTTCATTTTGTGAGAGTTCCTCTGAGAGTTCATCTTGTAGAGTTC 240
XX DB 181 TGTGCTGTCTGAGAGTTCATTTTGTGAGAGTTCCTCTGAGAGTTCATCTTGTAGAGTTC 240
XX
XX QY 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTGTAGTTCGTTG 300
XX DB 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTGTAGTTCGTTG 300
XX
XX QY 301 CCTTCTCCAGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX DB 301 CCTTCTCCAGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX
XX QY 361 CATAGTTTCTGCTAGTGGACCGT 385
XX DB 361 CATAGTTTCTGCTAGTGGACCGT 385
XX
XX RESULT 4
XX ABS71212 standard; cdNA; 385 BP.
XX
XX AC ABS71212;
XX
XX XX 27-NOV-2002 (first entry)
XX
XX DE Human prostate tumour protein partial DNA sequence #67.
XX
XX KW Human; immunogenic; prostate protein; prostate tumour protein;
XX prostate cancer; cytostatic; vaccine; ss.
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09/119,453

```
XX Homo sapiens.
XX OS US2002090372-A1.
XX PN 11-JUL-2002.
XX PD
XX
XX 14-JUL-1998; 98US-00115453.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX
XX (XUJU/) XU J.
XX (DILL/) DILLON D C.
XX
XX Xu J, Dillon DC;
XX
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 12; Page 40; 101pp; English.
XX
XX The present invention relates to a new polypeptide comprising an
XX immunogenic portion of a prostate protein. The invention is useful for
XX inhibiting the development of prostate cancer in a patient. The invention
XX is also useful as markers for diagnosing prostate cancer and for
XX monitoring diseases progression in patients. The present nucleic acid
XX sequence represents a DNA sequence that is part of a gene encoding a
XX human prostate tumour protein
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 3; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX
XX QY 61 GGTGGGACAGCCAGCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
XX DB 61 GGTGGGACAGCCAGCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
XX
XX QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX
XX QY 181 TGTGCTGTCTGAGAGTTCATTTTGTGAGAGTTCCTCTGAGAGTTCATCTTGTAGAGTTC 240
XX DB 181 TGTGCTGTCTGAGAGTTCATTTTGTGAGAGTTCCTCTGAGAGTTCATCTTGTAGAGTTC 240
XX
XX QY 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTGTAGTTCGTTG 300
XX DB 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTGTAGTTCGTTG 300
XX
XX QY 301 CCTTCTCCAGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX DB 301 CCTTCTCCAGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX
XX QY 361 CATAGTTTCTGCTAGTGGACCGT 385
XX DB 361 CATAGTTTCTGCTAGTGGACCGT 385
XX
XX RESULT 5
XX AAH93423
XX ID AAH93423 standard; cdNA; 385 BP.
XX
XX XX
```

```
AC AAH93423;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P80 (also P740P).
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytotatic; gene therapy; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO200151633-A2.
XX
XX 19-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US001574.
XX
XX 14-JAN-2000; 2000US-00483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
XX Claim 1; Page 250; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. (I)
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 385; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCGCCAGCACTTTAGGATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCGCCAGCACTTTAGGATGCTGA 60
QY 61 GGTCCGACGAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTCCGACGAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCGTTTAAAAAGGGAGCTTCTTTAAAAAGAGTCTTAGCCACGATTTGTGTAGAGCAGC 180
DB 121 CCGTTTAAAAAGGGAGCTTCTTTAAAAAGAGTCTTAGCCACGATTTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACATTTTGTGAGAGATTTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTCACATTTTGTGAGAGATTTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGCTTGGACATGAGATGGGCTGTGATCTGATCTCAGCACTCTTGTGCTG 300
DB 241 CTGGGCGAGCTTGGACATGAGATGGGCTGTGATCTGATCTCAGCACTCTTGTGCTG 300
```

```
QY 301 CCTCTCCAGGGCCCGAGCCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCGAGCCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGACCGT 385

RESULT 6
AAS63515
ID AAS63515 standard; cDNA; 385 BP.
XX
XX AAS63515;
AC
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #67.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200173032-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 27-MAR-2001; 2001WO-US009919.
PF
XX
XX 27-MAR-2000; 2000US-00536857.
PR
XX
XX 09-MAY-2000; 2000US-00568100.
PR
XX
XX 12-MAY-2000; 2000US-00570737.
PR
XX
XX 13-JUN-2000; 2000US-00593793.
PR
XX
XX 27-JUN-2000; 2000US-00605783.
PR
XX
XX 09-AUG-2000; 2000US-00636215.
PR
XX
XX 29-AUG-2000; 2000US-00651236.
PR
XX
XX 06-SEP-2000; 2000US-00657279.
PR
XX
XX 02-OCT-2000; 2000US-00679426.
PR
XX
XX 10-OCT-2000; 2000US-00685166.
PR
XX
XX 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
PT
XX
XX Claim 1; Page 252; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 385; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCAGACACTTTTCCAGCACCTTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTTCCAGCACCTTTTAGGAATGCTGA 60
QY 61 GGTGGACCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATCAGGTCTGAGAGTTC 120
DB 61 GGTGGACCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTGAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTGAGAGCAGC 180
QY 181 TGTGCTGTCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300
DB 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360
QY 361 CATAGTTTCTGTCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 7

AAH02488
ID AAH02488 standard; cDNA; 385 BP.
XX
AC AAH02488;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA sequence for P80.
XX

Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX

OS Homo sapiens.
XX

FN WO200125272-A2.
XX

PD 12-APR-2001.
XX

XX 04-OCT-2000; 2000WO-US027464.
XX

XX 04-OCT-1999; 99US-0157455P.
XX

XX (CORI-) CORIXA CORP.
XX

XX Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX

XX WPI; 2001-245062/25.
XX

XX Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX

XX Claim 50; Page 141; 276pp; English.
XX

XX The present invention describes an isolated polypeptide (I) comprising at
XX least an immunogenic portion of a prostate tumour antigen protein or its
XX variant. (I) have cytostatic activity and can be used in vaccine
XX production. (II, prostate tumour antigen polynucleotides, an antigen
XX presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
XX pharmaceutical composition containing (I) are useful for inhibiting the
XX development of cancer in a patient. Antibodies specific for prostate
XX specific proteins and oligonucleotides that hybridize to a polynucleotide
XX that encodes a prostate specific protein are useful for detecting the

CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention
XX

SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 4; Length 385;
Best Local Similarity 100.0%; Pred No. 1.8e-117;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTTGTGAGACACTTTTCCAGCACCTTTTAGGAATGCTGA 60

DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTTGTGAGACACTTTTCCAGCACCTTTTAGGAATGCTGA 60

QY 61 GGTGGACCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATCAGGTCTGAGAGTTC 120

DB 61 GGTGGACCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTGAGAGCAGC 180

DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTGAGAGCAGC 180

QY 181 TGTGCTGTCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240

DB 181 TGTGCTGTCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300

DB 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360

DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTCTAGTGGACCGT 385

DB 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 8

AAH84737
ID AAH84737 standard; cDNA; 385 BP.
XX

AC AAH84737;
XX

XX 25-SEP-2001 (first entry)
XX

XX Human prostate-specific cDNA sequence P80.
XX

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX

XX Homo sapiens.
XX

XX WO200134802-A2.
XX

XX 17-MAY-2001.
XX

XX 09-NOV-2000; 2000WO-US030904.
XX

XX 12-NOV-1999; 99US-00439313.
XX

XX 18-NOV-1999; 99US-00443686.
XX

XX (CORI-) CORIXA CORP.
XX

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX

XX WPI; 2001-308785/32.
XX

XX Isolated polypeptide comprising at least an immunogenic portion of a
PT

PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
PS Claim 31; Page 150; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
Query Match 100.0%; Score 385; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACATCCACTTCCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA 60
DB 1 ACTACACACATCCACTTCCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA 60
QY 61 GGTCCGACGACGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTCCGACGACGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTGTGCTTG 300
DB 241 CTGGGCGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTGTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385
RESULT 9
AAF86939
ID AAF86939 standard; cDNA; 385 BP.
XX
AC AAF86939;
XX
XX 06-JUL-2001 (first entry)
DT
DE Human P704P inventive antigen coding sequence SEQ ID NO: 334.
XX
XX Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor; ss.
KW
XX Homo sapiens.
OS
XX WO200125273-A2.
PN
XX 12-APR-2001.
PD
XX 04-OCT-2000; 2000WO-US027465.
PF

XX 04-OCT-1999; 99US-0157459P.
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX WPI; 2001-328324/34.
XX
XX Polypeptide comprising part of the Wilm's Tumor gene product sequence is
XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
XX and cancer associated with WTI.
XX
XX Disclosure; Page 213-214; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a coding sequence used in the exemplification of the invention
XX
SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
Query Match 100.0%; Score 385; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACATCCACTTCCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA 60
DB 1 ACTACACACATCCACTTCCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA 60
QY 61 GGTCCGACGACGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTCCGACGACGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTGTGCTTG 300
DB 241 CTGGGCGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTGTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385
RESULT 10
ACA59324
ID ACA59324 standard; cDNA; 385 BP.
XX
XX ACA59324;
XX
XX 10-JUN-2003 (first entry)
DT
DE Prostate cancer therapy associated cDNA #67.
XX
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.

XX OS Homo sapiens.
XX US2002192763-A1.
XX PD 19-DEC-2002.
XX
XX 29-JUN-2001; 2001US-00895793.
XX PF 04-OCT-1999; 99US-0157455P.
XX PR 04-OCT-2000; 2000US-00679272.
XX PR 28-MAR-2001; 2001US-00822827.
XX
XX (XUJJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (HURA/) HURAL J.
XX (MCNE/) MCNEILL P D.
XX (HOUG/) HOUGHTON R L.
XX (DBAS/) Y DE BASSOLS C V.
XX (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
XX WPI; 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
XX Example 3; SEQ ID NO 67; 85pp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 385; DB 5; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGGACCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

Db 61 GGTGGGACCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGAGTTCCTCTCGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGAGTTCCTCTCGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACCTCCTTAGTCTGCTTG 300
Db 241 CTGGGCGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACCTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTCTGTCACAGGGCAGCTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTCTGTCACAGGGCAGCTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
RESULT 11
AAS10066
ID AAS10066 standard; cDNA; 385 BP.
XX AC AAS10066;
XX DT 24-OCT-2001 (first entry)
XX DE Human prostate tumour cDNA P86 #4.
XX KW Human; prostate tumour protein; prostate cancer; ss.
XX OS Homo sapiens.
XX PN US6262245-B1.
XX PD 17-JUL-2001.
XX PF 25-FEB-1998; 98US-00030607.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 09-FEB-1998; 98US-00020956.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC;
XX WPI; 2001-440862/47.
XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumor protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient.
XX
XX Example 2; Col 81; 105pp; English.
XX The sequence is a human prostate tumour cDNA which encodes a partial
CC tumour protein. The DNA is useful for inhibiting the development of
CC prostate cancer or for treating prostate cancer in a patient
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 385; DB 5; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATGCTGA 60

09/030, 687

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
DB |||||||
61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAGGGGACTTGCTTAAAGAGAGCTAGCCAGATTGTGAGAGCAGC 180
DB |||||||
121 CCCTTTTAAAGGGGACTTGCTTAAAGAGAGCTAGCCAGATTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
DB |||||||
181 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
DB |||||||
241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATAC 360
DB |||||||
301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB |||||||
361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 12

ABL94887

ID ABL94887 standard; cDNA; 385 BP.

XX ABL94887;

AC ABL94887;

XX

19-JUL-2002 (first entry)

DE Human P80 cDNA sequence SEQ ID NO 67.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.

XX Homo sapiens.

OS US2002022248-A1.

PN 21-FEB-2002.

XX

PF 12-JAN-2001; 2001US-00759143.

XX

PR 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 10-FEB-1998; 98US-00020956.

PR 25-FEB-1998; 98US-00030607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00159812.

PR 15-JAN-1999; 99US-00232149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00483672.

PR 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 10-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00685166.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MIT/) MITCHAM J L.

PA

PA (HAR/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 1; SEQ ID NO 67; 87pp; English.

CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention

XX SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACATCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB |||||||
1 ACTACACACATCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACCCGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
DB |||||||
61 GGTGGACCCGACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAGGGGACTTGCTTAAAGAGAGTCTAGCCAGATTGTGAGAGCAGC 180
DB |||||||
121 CCCTTTTAAAGGGGACTTGCTTAAAGAGAGTCTAGCCAGATTGTGAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
DB |||||||
181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTTGACATGAGATGGGCTGCTGATCTCAGCACTCCTTAGTCTGCTTG 300
DB |||||||
241 CTGGGAGCTTTGACATGAGATGGGCTGCTGATCTCAGCACTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATAC 360
DB |||||||
301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB |||||||
361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 13

ABS58596

ID ABS58596 standard; cDNA; 385 BP.

XX

AC ABS58596;

XX

DT 05-NOV-2002 (first entry)
XX Prostate tumour cDNA #67.
DE Human; prostate tumour; immunotherapy; prostate cancer; gene; ss.
XX Homo sapiens.
OS
XX US2002081580-A1.
XX 27-JUN-2002.
XX
XX 25-FEB-1998; 98US-00030606.
XX
XX 25-FEB-1997; 97US-00806596.
PR 01-AUG-1997; 97US-00904809.
PR 09-FEB-1998; 98US-00020747.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
XX
XX Xu J, Dillon DC;
PI
XX WPI; 2002-607662/65.
DR
XX
XX Detecting prostate cancer comprises contacting a sample with an agent
PT capable of binding to a polypeptide with an immunogenic portion of a
PT prostate protein, oligonucleotide primers or a probe specific for DNA
PT encoding the polypeptide.
XX
XX Claim 1; Page 42-43; 11pp; English.
PS
XX The invention relates to a method of detecting prostate cancer by
CC contacting a biological sample from a patient with: (a) a binding agent
CC that binds to a polypeptide having an immunogenic portion of a prostate
CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the
CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);
CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the
CC polypeptide of (a). The method and polypeptides are useful for
CC diagnosing, treating, particularly by immunotherapy, monitoring the
CC progression, and inhibiting the development of prostate cancer in a
CC patient. The polypeptides may be used to generate antibodies useful
CC for the diagnosis and monitoring of prostate cancer. AB58530-AB58746
CC represent human prostate tumour cDNA sequences of the invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC 120
DB 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGAGAGTTCATCTTTTGTGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGTTCATCTTTTGTGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTGTGCATGATGAGTGGGGCTGGTCTGATCTCAGCACTCTTCTGCTTG 300
DB 241 CTGGGAGCTTGTGCATGATGAGTGGGGCTGGTCTGATCTCAGCACTCTTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCCTTGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCCTTGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360

Db 301 CCTCTCCAGGGCCCCAGCCTTGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGTAGTGGACCGT 385

RESULT 14
ACC95051
ID ACC95051 standard; cDNA; 385 BP.
XX
XX ACC95051;
XX
XX 28-AUG-2003 (first entry)
XX Prostate tumour specific cDNA sequence SEQ ID 67.
DE
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Bassols, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
DR
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX Example 3; Page 317; 691pp; English.
PS
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 385; DB 8; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC 120
DB 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180

```
QY 181 TGTGCTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Db 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 15
ADBI3517
ID ADBI3517 standard; cDNA; 385 BP.
XX
AC ADBI3517;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA P80/P704P.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
(PCORI-) CORIXA CORP.
XX
```

```
PI Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 3; Page; 101pp; English.
XX
CC The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is one of the
CC disclosed human prostate specific cDNAs. Note: Except where otherwise
CC indicated, the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACATCCACTTGGCCCTTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACATCCACTTGGCCCTTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACCCACCATCTCATGTGCAAGATTGCCAGCAGACATCATGTTAGAGTTC 120
Db 61 GGTGGACCCACCATCTCATGTGCAAGATTGCCAGCAGACATCATGTTAGAGTTC 120
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCCTCTGTAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCCTCTGTAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300
Db 241 CTGGGCACTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGCACTCTCAGATGCCCATAC 360
```


|||||
301 CCTCTCCAGGGCCCCAGCCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
|||||
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Search completed: December 31, 2006, 12:54:17
Job time : 300.256 secs

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:13:09 ; Search time 2478.7 Seconds
(without alignments)
9932.518 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactccacttgc.....tttctgtgtagtgacogt 385

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_htg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	2	BD070216
2	385	100.0	385	2	BD241980
3	385	100.0	385	2	AR237163
4	385	100.0	385	2	AR278187
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6	385	100.0	385	2	AR370779
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8	385	100.0	385	2	AR399919
9	385	100.0	385	2	AR405186
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34	348.2	90.4	182216	12	AC182114
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38	313.6	81.5	132753	5	AC131180
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ALIGNMENTS

RESULT 1
BD070216

LOCUS
DEFINITION

Compounds for immunodiagnosis of prostate cancer and methods for their use. linear PAT 27-AUG-2002

ACCESSION
BD070216

VERSION
BD070216.1 GI:22615819

KEYWORDS
JP 2001513886-A/67.

SOURCE
Homo sapiens

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo

REFERENCE
1 (bases 1 to 385)

AUTHORS
Xu,J. and Dillon,D.C.

TITLE
Compounds for immunodiagnosis of prostate cancer and methods for their use

JOURNAL
Patent: JP 2001513886-A 67 04-SEP-2001;

COMMENT
CORIXA CORP

OS
Homo sapiens (human)

PN
JP 2001513886-A/67

PD
04-SEP-2001

PR
25-FEB-1998 JP 1998537008

PF
25-FEB-1997 US 08/806596,01-AUG-1997 US 08/904809 PR

PI
JIANGCHUN XU,DAVIN C DILLON

PC
GO1N33/574,GO1N33/577,C07K16/30,A61K39/395,A61K47/48,C12Q1/68,

CC
Strandedness: Single;

CC
Topology: Linear;

CC
Compounds for immunodiagnosis of prostate cancer and methods for their use

CC
Compounds for immunodiagnosis of prostate cancer and methods for their use

FT
Key

Location/Qualifiers

1..385

/organism='Homo sapiens (human)'

Location/Qualifiers

1..385

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/db_xref='taxon:9606'

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2
BD241980 385 bp DNA linear PAT 17-JUL-2003
LOCUS Compounds for immunotherapy and diagnosis of prostate cancer and
DEFINITION methods for their use.
ACCESSION BD241980
VERSION BD241980.1 GI:33051750
KEYWORDS JP 2002520054-A/67.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 385)
Dillon,D.C., Harlocker,S.L., Yuqiu,J., Xu,J. and Mitcham,J.L.
Compounds for immunotherapy and diagnosis of prostate cancer and
methods for their use
Patent: JP 2002520054-A 67 09-JUL-2002;
CORIXA CORP
OS Homo sapiens (human)
PN JP 2002520054-A/67
PF 09-JUL-2002
PI 14-JUL-1999 JP 2000560247
PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR
09-APR-1999 US 09/288946
PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI
JIANGCHUN XU,
PI JENNIFER LYNN MITCHAM
PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,
PC C12N5/10,
PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
PC A61K37/02,
PC C12N5/00
CC Compounds for immunotherapy and diagnosis of prostate cancer
and methods
CC for their use Location/Qualifiers
FH Key

FT source 1. .385
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
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Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3
AR237163 385 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 67 from patent US 6465611.
DEFINITION AR237163
ACCESSION AR237163
VERSION AR237163.1 GI:27281821
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for
their use
JOURNAL Patent: US 6465611-A 67 15-OCT-2002;
Corixa Corporation; Seattle, WA
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
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Db 61 GGTGGACCCAGCCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
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Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 4
LOCUS AR278187 385 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 67 from patent US 6512094.
ACCESSION AR278187
VERSION AR278187.1 GI:29712433
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 67 28-JAN-2003;
CORIXA Corporation; Seattle, WA
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360
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Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385
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LOCUS AR366883 385 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 67 from patent US 6329505.
ACCESSION AR366883
VERSION AR366883.1 GI:34599858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J., Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and Day, C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6329505-A 67 11-DEC-2001;
CORIXA Corporation; Seattle, WA
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
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Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385
RESULT 6
LOCUS AR370779 385 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 67 from patent US 6395278.
ACCESSION AR370779
VERSION AR370779.1 GI:34607672
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yugu,J.
TITLE        Prostate specific fusion protein compositions
JOURNAL      Patent: US 6395278-A 67 28-MAY-2002;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385
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RESULT 8
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LOCUS        AR399919
DEFINITION   Sequence 67 from patent US 6620922.
ACCESSION    AR399919
VERSION      AR399919.1 GI:40142815
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
              Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
              Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
              Hepler,W.T. and Henderson,R.A.
              Compositions and methods for the therapy and diagnosis of prostate
              cancer
              Patent: US 6620922-A 67 16-SEP-2003;
              Corixa Corporation; Seattle, WA
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RESULT 7
AR392284
LOCUS        AR392284
DEFINITION   Sequence 67 from patent US 6613872.
ACCESSION    AR392284
VERSION      AR392284.1 GI:40116293
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Xu,J. and Dillon,D.C.
TITLE        Compounds for immunotherapy of prostate cancer and methods for
              their use
JOURNAL      Patent: US 6613872-A 67 02-SEP-2003;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
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RESULT 8
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ACCESSION    AR399919
VERSION      AR399919.1 GI:40142815
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
              Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
              Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
              Hepler,W.T. and Henderson,R.A.
              Compositions and methods for the therapy and diagnosis of prostate
              cancer
              Patent: US 6620922-A 67 16-SEP-2003;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 385; DB 2; Length 385;
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Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGACCGT 385
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JOURNAL Patent: US 6759515-A 67 06-JUL-2004;
FEATURES Corixa Corporation; Seattle, WA
source Location/Qualifiers
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/mol_type="genomic DNA"

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Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGCCCAGCACATTTAGGAATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGCCCAGCACATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
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QY 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
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QY 241 CTGGGCACTCTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
DB 241 CTGGGCACTCTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTTACAGGGCACTCTCAGATGCCCATAC 360
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 13
AR605372 AR605372 385 bp DNA linear PAT 15-DEC-2004
LOCUS Sequence 67 from patent US 6818751.
DEFINITION AR605372
ACCESSION AR605372
VERSION AR605372.1 GI:56657036
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
TITLE
JOURNAL Patent: US 6818751-A 67 16-NOV-2004;
Corixa Corporation; Seattle, WA
FEATURES Location/Qualifiers
source 1..385
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ORIGIN
Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
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QY 241 CTGGGCACTCTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
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QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTTACAGGGCACTCTCAGATGCCCATAC 360
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 12
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LOCUS Sequence 67 from patent US 6800746.
DEFINITION AR588552
ACCESSION AR588552
VERSION AR588552.1 GI:56635449
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
TITLE
JOURNAL Patent: US 6800746-A 67 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES Location/Qualifiers
source 1..385
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGCCCAGCACATTTAGGAATGCTGA 60
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 14
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LOCUS AR652986 385 bp mRNA linear PAT 13-JUN-2005
DEFINITION Sequence 67 from patent US 6887660.
ACCESSION AR652986
VERSION AR652986.1 GI:67583223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 385)
AUTHORS Xu, J. and Dillon, D. C.
TITLE Compounds for immunodiagnosis of prostate cancer and methods for their use
JOURNAL Patent: US 6887660-A 67 03-MAY-2005;
Corixa Corporation; Seattle, WA
FEATURES
source Location/Qualifiers
1..385
/organism="unknown"
/mol_type="mRNA"

ORIGIN
Query Match 100.0%; Score 385; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGCACTTTTAGGAATGCTGA 60
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 15
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LOCUS AR656711 385 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 67 from patent US 6894146.
ACCESSION AR656711
VERSION AR656711.1 GI:67589779
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 385)
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedwick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6894146-A 67 17-MAY-2005;
Corixa Corporation; Seattle, WA
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGCACTTTTAGGAATGCTGA 60
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QY 301 CCTCTCCAGGGCCCGAGCTGCGCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCGAGCTGCGCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
6976.201 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_hic:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gsa1:*
- 12: gb_gsa2:*
- 13: gb_gsa3:*
- 14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	312.8	81.2	556	9	DB045159
2	231.8	60.2	986	3	BQ068886
3	112.4	29.2	861	5	CD251924
4	111.8	29.0	491	9	DN920910
5	107.4	27.9	5483	6	BC063888
6	101.8	26.4	6098	6	HSM809270
7	100.8	26.2	553	9	DA554900
8	95	24.7	986	3	BQ068886
9	93.4	24.3	873	5	CD251853
10	84.2	21.9	660	14	AG106788
11	83.8	21.8	6098	6	HSM809270
12	77.4	20.1	628	14	AG065887
13	74.4	19.3	704	14	AG094252
14	74.2	19.3	861	8	CR748036
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17	73	19.0	697	4	BX954640
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19	72.2	18.8	863	11	AQ741520

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21	70.2	18.2	559	2	BM315072
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23	70	18.2	674	14	AG064313
24	69.8	18.1	680	14	AG095806
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26	69	17.9	424	11	AQ426607
27	69	17.9	740	14	AG098047
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29	68.6	17.8	489	7	BE159477
30	68.4	17.8	517	11	AQ402468
31	68.4	17.8	889	13	C2461627
32	68.2	17.7	556	9	DB045159
33	68	17.7	479	11	AQ227716
34	68	17.7	593	1	AV688475
35	67.6	17.6	623	14	AG079180
36	67.6	17.6	661	14	AG054439
37	67.2	17.5	440	11	AQ818967
38	67.2	17.5	654	14	AG093794
39	67	17.4	756	14	CR960558
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ALIGNMENTS

RESULT 1	DB045159	TEST12 Homo sapiens	556 bp	mRNA	linear	EST 11-NOV-2005
DB045159	sequence.					
LOCUS	DB045159					
DEFINITION	DB045159.1	GI:82061582				
ACCESSION	DB045159					
VERSION	EST.					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 556)					
AUTHORS	Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.					
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes					
JOURNAL	Genome Res. 16 (1), 55-65 (2006)					
PURMED	16344560					
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com					
FEATURES	NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.					
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 /clone="TES112033322"
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 /note="Vector: pME18SFL3"

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Query Match 81.2%; Score 312.8; DB 9; Length 556;
 Best Local Similarity 92.4%; Pred. No. 4.2e-83;
 Matches 340; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
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 Db TCTACTTGCCCTTGTGAGACACTTATCCAGCAGCTTTAGGAATGCTGAGTCCATACCAG 248
 Qy 72 CCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCCTGAGAGTTCCCTTTTAAAA 131
 Db CCACATCTCATGTGCAAGATTGCCAGCAGAGATCAGGTCCAGAGATTTCTTGTTTAAAA 308
 Qy 132 AAGGGAGCTTGTCTTAA-AAAAGAAGCTAGCCAGCAATTTGTAGAGCAGCTGTGCTGTGC 190
 Db AAGGGAGCTTGTCTTAAATAAAGAAGCTTGGCCATGTTTGTGTAGAGCAGCTGTGCTGTGC 368
 Qy 191 TGGAGATTCACCTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGGCTGGGCGATC 250
 Db TGGGGGTTACCTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTCTGGAGGCTGGGCGATC 428
 Qy 251 TTGCACATGAGATGGGGTGTGCTGATCTCAGCAGCTCTCTTGTGCTTGTGCTCTCCAG 310
 Db TTGCACATGAGATGGGGTGTGCTGATGGCAGCAGCTCTTGTGCTTGTGCTCTCCAT 488
 Qy 311 GGCCCCAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCATACATAGTTTCT 370
 Db GGCCCCAGCTGGCCACACATGCTTACAGGGCAGCTCTTGTAGTGGCCACATATAGCTTCC 548
 Qy 371 GTGCTAGT 378
 Db GTGCTAGT 556

RESULT 2

BQ068886/c
 LOCUS BQ068886 986 bp mRNA linear EST 02-APR-2002
 DEFINITION AGENCOURT_6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802737
 5', mRNA sequence.
 ACCESSION BQ068886
 VERSION BQ068886.1 GI:19897932
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 986)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM2037 row: j column: 18
 High quality sequence stop: 751.
 Location/Qualifiers
 1..986
 /organism="Homo sapiens"
 /mol_type="mRNA"
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FEATURES

source

/clone="IMAGE:5802737"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_47"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 60.2%; Score 231.8; DB 3; Length 986;
 Best Local Similarity 88.0%; Pred. No. 1.6e-58;
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 Qy 131 AAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGATTTGTGTAGAGCAGCTGTGCTGTGC 190
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 Db TGGAGATTCACCTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGCTGGGCGATC 179
 Qy 251 TTGCACATGAGATGGGGTGTGCTGATCTCAGCAGCTCTCTAGTCTGCTTGTGCTCTCCAG 310
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 Qy 311 G 311
 Db 118 G 118

RESULT 3
 LOCUS CD251924 861 bp mRNA linear EST 22-MAY-2003
 DEFINITION AGENCOURT_14204354 NIH_MGC_180 Homo sapiens cDNA clone
 IMAGE:30383087 5', mRNA sequence.
 ACCESSION CD251924
 VERSION CD251924.1 GI:31012390
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 861)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDAM446 row: f column: 24
High quality sequence stop: 701.

FEATURES

Location/Qualifiers
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/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
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/notes="Organ: testis; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 29.2%; Score 112.4; DB 5; Length 861;
Best Local Similarity 99.1%; Pred. No. 2e-22;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 272 TCTGATCTCAGCACTCTTAGTCTGCTTCCAGGCGCCAGCCTGCGCCACACCT 331
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Db 560 TCTGATCTCAGCACTCTTAGTCTGCTTCCAGGCGCCAGCCTGCGCCACACCT 619
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QY 332 GCTTACAGGCACTCTCAGATGCCATACATAGTTTCTGCTAGTGACCGT 385
|||||
Db 620 GCTTACAGGCACTCTCAGATGCCATACATAGTTTCTGCTAGTGACCGT 673
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RESULT 4

DN920910 491 bp mRNA linear EST 20-OCT-2005
LOCUS MCF7RNA28P21TR Human MCF7 breast cancer cell line near full length
DEFINITION normalized library (MCF7 EST) Homo sapiens cDNA clone
MCF7 RNA_L_28_P21, mRNA sequence.
ACCESSION DN920910 GI:77951595
VERSION DN920910.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 491)

REFERENCE
AUTHORS Volik, S.V., Raphael, B.J., Huang, G.-Q., Murnane, J., Brebner, J.H.,
Bajzarowicz, K., Paris, P., Tao, Q., Kowbel, D., Lapuk, A.V., Kuo, W.-L.,
Shagin, D.A., Shagina, I.A., Magrane, G., Gray, J.W., Jan, F.-C., de
Jong, P., Pevzner, P. and Collins, C.
Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab

JOURNAL

COMMENT UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7067
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
Seq primer: SP6 5'-ATTAGTGACACTAGATGATAC-3'.
Location/Qualifiers
1. .491

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MCF7_RNA_L_28_P21"
/sex="female"
/cell_line="MCF7"
/clone_lib="Human MCF7 breast cancer cell line near full
length normalized library (MCF7 EST)"
/note="Vector: pAL17; This library was constructed from

ORIGIN

Query Match 29.0%; Score 111.8; DB 9; Length 491;
Best Local Similarity 90.2%; Pred. No. 2.7e-22;
Matches 119; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 254 CACATGAGATGGGGTGGTCTGATCTCAGCACTCTTAGTCTGCTGCTCTCCAGGGC 313
|||||
Db 353 CACATGAGATGGGGTGGTCTGATGCGCACTCTCTTANTCTGTTGCTCTCCATGGC 412
|||||
QY 314 CCCAGCTGGCCACACCTGCTTACAGGCGCACTCTCAGATGCCATACATAGTTTCTGTG 373
|||||
Db 413 CTTAGCTGGCCACACATCTTACAGGCGCACTCTTAGATGCCACACTAGTCTGCCGTG 472
|||||
QY 374 CTATGGACCGT 385
|||||
Db 473 CTATGGACCTGT 484
|||||

RESULT 5

BC063888 5483 bp mRNA linear HTC 09-DEC-2005
LOCUS Homo sapiens prostate-specific P704P mRNA, cDNA clone
DEFINITION IMAGE:30389199), with apparent retained intron.
ACCESSION BC063888
VERSION BC063888.1 GI:39645658
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 5483)

REFERENCE

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
Ackerman, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 5483)

CONSRMT

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSRMT
TITLE
JOURNAL
REMARK
COMMENT
NIH MGC Project
Direct Submission
Submitted (08-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Genome Sequence Centre,

MCF7 breast cancer cell line by Evrogen JSC.
(<http://www.evrogen.com>) using their standard procedure.
See http://shark.ucsf.edu/~stas/report_MCF7.pdf for
details."

```

BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kiehl Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smailus, Jeff Scott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 141 Row: 0 Column: 10
This clone has the following problem: retained intron.

FEATURES
source
Location/Qualifiers
1..5483
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30389199"
/tissue_type="Testis"
/clone_lib="NIH MGC_180"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6.1"

ORIGIN
Query Match 27.9%; Score 107.4; DB 6; Length 5483;
Best Local Similarity 99.1%; Pred. No. 1.1e-20;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 277 TCTCAGCACTCTTGTAGTCTGCTCTCCAGGCCCCAGCTGGCCACACCTGCTTA 336
|||
Db 3936 TCCAGCACTCTTGTAGTCTGCTCTCCAGGCCCCAGCTGGCCACACCTGCTTA 3995
|||

Qy 337 CAGGCACTCTCAGATGCCATACATAGTTCTGTCTAGTGACCGT 385
|||
Db 3996 CAGGCACTCTCAGATGCCATACATAGTTCTGTCTAGTGACCGT 4044
|||

RESULT 6
HSM809270/c HSM809270 Homo sapiens mRNA 6098 bp linear HTC 20-JAN-2005
LOCUS HSM809270
DEFINITION Homo sapiens mRNA; cDNA DKFP686J0529 (from clone DKFP686J0529).
ACCESSION BX649118
VERSION BX649118.1 GI:34368290
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 6098)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFP686J0529) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFP686J0529
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1..6098
/organism="Homo sapiens"

FEATURES
source
Location/Qualifiers
1..553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCHON2005010"
/cell_type="chondrocytes (HC)"
/note="Vector: pME18SFL3; primary culture, chondrocytes"

/mol_type="mRNA"
/db_xref="RZPD:DKFP686J0529Q"
/db_xref="taxon:9606"
/clone="DKFP686J0529"
/tissue_type="testis"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="putative transcript"

ORIGIN
Query Match 26.4%; Score 101.8; DB 6; Length 6098;
Best Local Similarity 93.8%; Pred. No. 5.4e-19;
Matches 106; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 248 GTCTTGCATGAGATGGGCTGTGTATCTCAGCACTCTTAGTGTGCTGCTTCC 307
|||
Db 5065 GTCTTGCATGAGATGGGCTGTGTATCTCAGCACTCTTAGTGTGCTTCC 5006
|||

Qy 308 CAGGCCCCAGCTGGCCACACCTGTCTAGGGCACTCTCAGATGCCATAC 360
|||
Db 5005 CAGGACCCAGCTGGCCACACCTGTCTAGGGCACTCTCAGATGCCATAC 4953
|||

RESULT 7
DA554900 DA554900 HCHON2 Homo sapiens cDNA clone HCHON2005010 5', mRNA
LOCUS DA554900
DEFINITION sequence.
ACCESSION DA554900
VERSION DA554900.1 GI:80884861
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 553)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1..553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCHON2005010"
/cell_type="chondrocytes (HC)"
/note="Vector: pME18SFL3; primary culture, chondrocytes"

ORIGIN

```

Query Match 26.2%; Score 100.8; DB 9; Length 553;
 Best Local Similarity 90.0%; Pred. No. 5.8e-19;
 Matches 108; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 240 GCTGGGAGCTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTT 299
 |||||
 Db 105 GCTGGGAGCTTTCACATGAGATGGAGCTGGTGTGCTCAGCCCTCCCTTAGTCTGCTT 164
 |||||
 QY 300 GCTCTCTCCAGGGCCCGAGCTGGCCACACTCTGTACAGGGCACTCTCAGATGCCCATTA 359
 |||||
 Db 165 GCCTCTCCAGGACCCGAGCTGGCCACACTGTCTACAGGGCACTCTCGGTGGCCACA 224
 |||||

RESULT 8
 BQ068886
 LOCUS BQ068886 986 bp mRNA linear EST 02-APR-2002
 DEFINITION AGENCOURT_6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802737
 5', mRNA sequence.

ACCESSION BQ068886
 VERSION BQ068886.1 GI:19897932
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 986)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgabbs-x@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM2037 row: j column: 18
 High quality sequence stop: 751.
 Location/Qualifiers

FEATURES

source
 1. 986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5802737"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_47"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 24.7%; Score 95; DB 3; Length 986;
 Best Local Similarity 65.1%; Pred. No. 3.8e-17;
 Matches 157; Conservative 0; Mismatches 80; Indels 4; Gaps 1;

QY 51 GGAATGCTGAGTGGACACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGT 110
 |||||
 Db 141 GGAGTCTGATATCAGACACGCCCATCTCATGTGAGGAGTCCCGCAGCAGATCAGGT 200
 |||||
 QY 111 CTGAGATTCCTCTTTTAAAAAGGGACCTTGCTTAAAAAGAGTCTAGCCACGATGT 170
 |||||
 Db 201 CTCAGAGGAGAACTGTCTCAAAAGTGAACCCCGGCACAGCATAGTGTCTTACACAAC 260
 |||||

QY 171 GTAGACAGCTGTGCTGTGAGATTCACATTTTGTGAGAGAGTTCTCTCTGAGACCTGA 230
 |||||
 Db 261 ATGCCCAGGCTCTTTTGTGAGCAAGTCCCTTTTGAAGAGGGAACTCTGGGAACTGA 320
 |||||
 QY 231 TCTTTAGAGCTGGGAGCTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTT 290
 |||||
 Db 321 TCTCT-----GCTGGGAGTCTTTGAACATGAGATGGGGCTGATCTGAATTCCTA 376
 |||||

QY 291 A 291
 Db 377 A 377

RESULT 9

CD251853 873 bp mRNA linear EST 22-MAY-2003
 AGENCOURT_14206078 NIH_MGC_180 Homo sapiens cDNA clone
 IMAGE:30383062 5', mRNA sequence.

ACCESSION CD251853
 VERSION CD251853.1 GI:31012319
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 873)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-r@mail.nih.gov

cDNA Library Preparation: Dr. Michael Brownstein
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDAM446 row: e column: 23
 High quality sequence stop: 540.
 Location/Qualifiers

FEATURES

source
 1. 873
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30383062"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_lib="NIH_MGC_180"
 /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
 Site 2: EcoRV (destroyed); Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.68 kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 24.3%; Score 93.4; DB 5; Length 873;
 Best Local Similarity 93.9%; Pred. No. 1.1e-16;
 Matches 108; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
 QY 272 TCTGATCTCAGCACTCTTTAGTCTGCTTCCCTCTCCAGGGCCCCAGCTGGCCACCT 331
 |||||
 Db 534 TCTGATCTCAGCACTCTTTAGTCTGCTTCCCTCTCCAGGGCCCCAGCTGGCCACCT 593
 |||||
 QY 332 GTTACAGGGCACTCTCA-GATGCCCATACCATAGTTTCTGTGCTAGTGACCGT 385
 |||||
 Db 594 GCTTACAGGGCACTCTCAGGGTGGCCCATACCATAGTTTCCGGGCCAGGGACCGT 648
 |||||

was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .628
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-055G12.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 20.1%; Score 77.4; DB 14; Length 628;
Best Local Similarity 74.2%; Pred. No. 7.2e-12;
Matches 115; Conservative 0; Mismatches 31; Indels 9; Gaps 1;
QY 240 GCTGGCAGCTTGCACATGAGATGGGCTGTGATCTCAGCACTCCTTAGTCTGCTT 299
DB 258 GCAGGGCAGCCTTGAACATCACCCTGGCTGTGCTGACCTGAGCACTCCTTGGTCTGCTG 199
QY 300 GCCTCTCCAGGGCCCGCCGCTGGCCACACCTGCTTACAGGGCACTCTCAG----- 350
DB 198 GCAAAATCTCTGGGGCCCGCCGCTGATCGCTTACAGTGCAGTCTCAGGTACCTTGA 139
QY 351 ATGCCCATACCATAGTCTTCTGTCTAGTGGACCGT 385
DB 138 AGCCCCACCATATCTTCTGTGCCAGTGGACCAT 104

RESULT 13

AG094252/c

LOCUS

AG094252 704 bp DNA linear GSS 03-NOV-2001

DEFINITION Pan troglodytes DNA, clone: PTB-094P10.R, genomic survey sequence.

ACCESSION

AG094252

VERSION

AG094252.1

GI:16646054

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pan.

REFERENCE

1

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,

Totoki, Y., Watanabe, H., and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 704)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,

Totoki, Y., Watanabe, H., and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: shuehiro@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/;

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of

clone tracking errors.

PRIMERS

Sequencing: M13Rev

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .704

FEATURES

source

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-094P10.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 19.3%; Score 74.4; DB 14; Length 704;
Best Local Similarity 77.6%; Pred. No. 6e-11; Mismatches 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 26; Indels 9; Gaps 0;
QY 240 GCTGGCAGCTTGCACATGAGATGGGCTGTGATCTCAGCACTCCTTAGTCTGCTT 299
DB 215 GCAGGTCACTTGCACATCAGTGGGCTGGCTGAAGTACCCCTATCTCTG 156
QY 300 GCCTCTCCAGGGCCCGCCGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCC 355
DB 155 GCCTCTCTCAGGGCCCTAGCCTGGCTGTGCTTGCAGGCGCAGCTTGAGTGCC 100

RESULT 14

CR748036/c

LOCUS

CR748036

DEFINITION

IMAGp998D104117; IMAGE:1623129 5', mRNA sequence.

ACCESSION

CR748036

VERSION

CR748036.1

GI:51661862

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 861)

Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.,

Peters, M., Radelof, U., and Schneider, D.

I.M.A.G.E. cDNA Clone Collection

Unpublished (2004)

CONTACT: Inge Ariart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD: IMAGp998D104117

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

CONTACT: Inge Ariart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCCACAGGAAACAGCTATGAC.

Location/Qualifiers

1. 861

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGp998D104117; IMAGE:1623129"

/clone_lib="Homo sapiens library (Ebert L)"

ORIGIN

Query Match 19.3%; Score 74.2; DB 8; Length 861;
Best Local Similarity 72.9%; Pred. No. 7.3e-11;
Matches 113; Conservative 0; Mismatches 33; Indels 9; Gaps 1;
QY 240 GCTGGCAGCTTGCACATGAGATGGGCTGTGATCTCAGCACTCCTTAGTCTGCTT 299
DB 194 GCCGGCAGCTTGTGCCATCGGGCAGGATGGTCCAACTTGAGAACACTTTGGTCTGCTG 135
QY 300 GCCTCTCCAGGGCCCGCCGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGC----- 354

Db 134 GCCTCTCTGGTCTCCAGCTGCGCACGCTCTTGACGGCAGCGCAGGTGCCTGG 75
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Db 74 GGGTCTCTCACCATAGCTTCTGCACCTGGTGGACCGT 40

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AQ784117	
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DEFINITION	HS_3034_B1_A11_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=21 Row=B, genomic survey sequence.
	527 bp DNA linear GSS 03-AUG-1999

ACCESSION
 AQ784117
 VERSION
 AQ784117.1 GI:5691741
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 527)
 REFERENCE
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 3034 row: B column: 21

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FEATURES
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    1. 527
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /clones="Plate=3034 Col=21 Row=B"
      /sex="male"
      /clone_lib="CIT Approved Human Genomic Sperm Library D"
      /note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
      F-Coli DH10B"
      High quality sequence stop: 527.
      Location/Qualifiers
        trabs: and ends

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Search completed: December 31, 2006, 19:30:49
Job time : 3091.06 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	385	100.0	385	3	US-09-759-143-67	Sequence 67, Appl
2	385	100.0	385	3	US-09-780-669-67	Sequence 67, Appl
3	385	100.0	385	3	US-09-030-606-67	Sequence 67, Appl
4	385	100.0	385	3	US-09-822-827-67	Sequence 67, Appl
5	385	100.0	385	3	US-09-115-453-67	Sequence 67, Appl
6	385	100.0	385	3	US-09-233-880-67	Sequence 67, Appl
7	385	100.0	385	3	US-09-895-793-67	Sequence 67, Appl
8	385	100.0	385	3	US-09-895-814-67	Sequence 67, Appl
9	385	100.0	385	6	US-10-012-896-67	Sequence 67, Appl
10	385	100.0	385	6	US-10-010-940-67	Sequence 67, Appl
11	385	100.0	385	7	US-10-144-678A-67	Sequence 67, Appl
12	385	100.0	385	7	US-10-294-025-67	Sequence 67, Appl
13	385	100.0	385	8	US-10-688-838-67	Sequence 67, Appl
14	385	100.0	385	16	US-11-234-786-67	Sequence 67, Appl
15	381.8	99.2	3710	7	US-10-294-025-1036	Sequence 1036, Ap
16	318.2	82.6	1177	6	US-10-198-846-11258	Sequence 11258, A
17	307.2	79.8	3218	16	US-11-234-786-701	Sequence 701, App

Db 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGCCCAGACACTTTAGAAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTCTCTCTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTCTCTCTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2

US-09-780-669-67

; Sequence 67, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-780-669-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGCCCAGCAGCTTTAGGAATGCTGA 60

Db 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGCCCAGCAGCTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTCTCTCTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTCTCTCTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
Db 241 CTGGCAGCTTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3

US-09-030-606-67

; Sequence 67, Application US/09030606

; Patent No. US20020081580A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F

; NUMBER OF SEQUENCES: 224

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/030,606

; FILING DATE: 25-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.428C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 67:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 385 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACTACACACACTCCACTTGCCTTGTGAGACACATTTGTGCCAGCACCTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGCCTTGTGAGACACATTTGTGCCAGCACCTTTAGGAATGCTGA	60
Qy	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC	120
Db	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC	120
Qy	121	CCCTTTTAAAAAGGGGACTTCTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGACGAC	180
Db	121	CCCTTTTAAAAAGGGGACTTCTCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGACGAC	180
Qy	181	TGTGCTGTGCTCGAGATTTCATTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAG	240
Db	181	TGTGCTGTGCTCGAGATTTCATTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAG	240
Qy	241	CTGGGCAGTCTTGACATGAGATGGGCTGTGCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Db	241	CTGGGCAGTCTTGACATGAGATGGGCTGTGCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Qy	301	CCTCTCCCAAGGGCCCCAGCCTTGCCACACCTTGCTTTACAGGGCACTCTCAGATGCCATAC	360
Db	301	CCTCTCCCAAGGGCCCCAGCCTTGCCACACCTTGCTTTACAGGGCACTCTCAGATGCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGGACCGT	385

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RESULT 4
US-09-822-827-67
; Sequence 67, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 382
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-67

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Query Match	100.0%	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 2.2e-126;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACTACACACATCCACTTGCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA	60	
Db	1	ACTACACACATCCACTTGCCTTGTGAGACACATTTGTCCAGCACATTTAGGAATGCTGA	60	
Qy	61	GGTGGGACGACCACATCTCATGTGCAAGATTGCCACGACACATCAGGCTCTGAGAGTTC	120	
Db	61	GGTGGGACGACCACATCTCATGTGCAAGATTGCCACGACACATCAGGCTCTGAGAGTTC	120	
Qy	121	CCCTTTTAAAAAGGGGACTTGGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGAGCAGC	180	
Db	121	CCCTTTTAAAAAGGGGACTTGGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGAGCAGC	180	
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Qy	241	CTGGGCGAGTCTTGACATGAGATGGGGCTGTCTGATCTCAGCACTCCTTAAGTCTGCCTTG	300	
Db	241	CTGGGCGAGTCTTGACATGAGATGGGGCTGTCTGATCTCAGCACTCCTTAAGTCTGCCTTG	300	
Qy	301	CCTCTCCAGGGGCCCGCCCTGGGCCACACCTGCTTTACAGGGGCACTCTCAGATGCCCATAC	360	

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Db      301 CCTCTCCAGGCCCCCAGCTGGGCCACACTTGCTTACAGGGCACCTCTCAGATGCCCATAC 360
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Db      361 CATAGTTTCTGTGCTAGTAGGCACCGT 385
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RESULT 5
US-09-115-453-67
; Sequence 67, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-67
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Qy	1	ACTACACACACTCCACTTGCCTTTGTGAGACACACTTTGTCCCGACGACTTTTAGGAATGCTGA	60		
Db	1	ACTACACACACTCCACTTGCCTTTGTGAGACACACTTTGTCCCGACGACTTTTAGGAATGCTGA	60		
Qy	61	GGTCGGACCGAGCCACATCTCATGTGCGAAGATTGCCACGACGACATCAGTCTGAGAGTTC	120		
Db	61	GGTCGGACCGAGCCACATCTCATGTGCGAAGATTGCCACGACGACATCAGTCTGAGAGTTC	120		
Qy	121	CCCTTTTAAAAAGGGGACCTTGCTTTAAAAAAGAGAGTCTAGCCACGATTGTGTAGAGCAGC	180		
Db	121	CCCTTTTAAAAAGGGGACCTTGCTTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC	180		
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTTAGAGG	240		
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTTAGAGG	240		
Qy	241	CTGGGCGAGTCTTGCACATGAGATGGGGCTGTCGTGATCTCAGCACCTCCTTAGTCTGCTTG	300		
Db	241	CTGGGCGAGTCTTGCACATGAGATGGGGCTGTCGTGATCTCAGCACCTCCTTAGTCTGCTTG	300		
Qy	301	CCTCTCCACGGGCCCCGACCTGGGCCACACCTGCTTTACAGGGGCACCTCTCAGATGCCCATAC	360		
Db	301	CCTCTCCACGGGCCCCGACCTGGGCCACACCTGCTTTACAGGGGCACCTCTCAGATGCCCATAC	360		
Qy	361	CATAGTTTCTGCTAGTGGACCGT	385		
Db	361	CATAGTTTCTGCTAGTGGACCGT	385		

RESULT 6
US-09-232-880-67
Sequence 67, Application US/09232880
Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232.880

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; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60

QY 61 GGTGGGACGACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTGGGACGACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAAGGGGACTTCTTAAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAAGGGGACTTCTTAAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGCACTTGGACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
DB 241 CTGGGCACTTGGACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCATAC 360
DB 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGAGACCGT 385

RESULT 7
US-09-895-793-67
; Sequence 67, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
DB 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60

QY 61 GGTGGGACGACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTGGGACGACGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAAGGGGACTTCTTAAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAAGGGGACTTCTTAAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGCACTTGGACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
DB 241 CTGGGCACTTGGACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCATAC 360
DB 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGAGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGAGACCGT 385

RESULT 8
US-09-895-814-67
; Sequence 67, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
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FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-67

Query Match 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTCA 60
DB 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTCA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGAGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
DB 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 9
US-10-012-896-67
Sequence 67, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-67

Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTCA 60
DB 1 ACTACACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTCA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGGATTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGAGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240
DB 181 TGTGCTGTGCTGAGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
DB 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 10
US-10-010-940-67
Sequence 67, Application US/10010940
Publication No. US2003008062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapien
US-10-010-940-67

Query Match 100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 11

US-10-144-678A-67

; Sequence 67, Application US/10144678A

; Publication No. US20030157089A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yudi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Hepler, William T.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals y de Bassols, Carlota

; APPLICANT: Foy, Teresa M.

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Deng, Ta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C28

; CURRENT APPLICATION NUMBER: US/10/144,678A

; CURRENT FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-144-678A-67

Query Match 100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 12

US-10-294-025-67

; Sequence 67, Application US/10294025

; Publication No. US20030185830A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C29

; CURRENT APPLICATION NUMBER: US/10/294,025

; CURRENT FILING DATE: 2002-11-12

; NUMBER OF SEQ ID NOS: 1038

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-294-025-67

Query Match 100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
Db 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 13
US-10-688-838-67
; Sequence 67, Application US/10688838
; Publication No. US20040141989A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D4
; CURRENT APPLICATION NUMBER: US/10/688,838
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-688-838-67

Query Match 100.0%; Score 385; DB 8; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60
Qy 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGACAGC 180
Db 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGACAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 14
US-11-234-786-67
; Sequence 67, Application US/11234786
; Publication No. US20060024301A1

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-67

Query Match 100.0%; Score 385; DB 16; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60
Qy 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
Qy 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGACAGC 180
Db 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGACAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
Qy 241 CTGGGAGCTTTCGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

Db 241 CTGGCAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 15

US-10-294-025-1036
; Sequence 1036, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1036
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1036
; LENGTH: 3710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-1036

Query Match 99.2%; Score 381.8; DB 7; Length 3710;
Best Local Similarity 99.5%; Pred. No. 8.4e-125;
Matches 383; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTTGCCCGACACTTTAGGAATGCTGA 60
Db 2282 ACCACACACTCCACTTGCCCTTGTGAGACACTTTTGCCCGACACTTTAGGAATGCTGA 2341
Qy 61 GGTCCGACAGCCACATCTCATGTCCAGATTGCCCGACAGACATCAGTCTGAGAGTTC 120
Db 2342 GGTCCGACAGCCACATCTCATGTCCAGATTGCCCGACAGACATCAGTCTGAGAGTTC 2401
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 2402 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 2461
Qy 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240
Db 2462 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 2521
Qy 241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 2522 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 2581
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Db 2582 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 2641
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 2642 CATAGTTTCTGTGCTAGTGGACCGT 2666

Search completed: December 31, 2006, 13:56:03
Job time : 615.045 secs

GenCore version 5.1.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03; Search time 557.33 Seconds
(without alignments)
6266.684 Million cell updates/sec

Title: US-09-232-880-107

Perfect score: 1621

Sequence: 1 cgcctggcactgcaggcca.....aaaaaaaaaaaaaaaaaaaa 1621

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA New:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US12_NEW_PUB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US13_NEW_PUB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US14_NEW_PUB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US15_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1621	100.0	1621	7	US-11-344-932-107
2	1621	100.0	1621	10	US-11-349-541-107
3	1574.2	97.1	2005	8	US-11-266-748A-23190
4	1574.2	97.1	2005	10	US-11-343-797-104
5	1571	96.9	2041	8	US-11-266-748A-22797
6	1524.8	94.1	2068	8	US-11-266-748A-23899
7	1240.6	76.5	2373	8	US-11-266-748A-57286
8	882.2	54.4	971	8	US-11-266-748A-215905
9	882.2	54.4	971	8	US-11-266-748A-237887
10	783	48.3	958	8	US-11-266-748A-46436
11	734.6	45.3	924	8	US-11-266-748A-84584
12	734.6	45.3	924	8	US-11-266-748A-111891
13	734.6	45.3	924	8	US-11-266-748A-137395
14	515	31.8	537	7	US-11-344-932-74
15	515	31.8	537	10	US-11-349-541-74
16	514	31.7	554	8	US-11-266-748A-349470
17	514	31.7	554	8	US-11-266-748A-432849
18	513.6	31.7	932	8	US-11-266-748A-371009
19	513.6	31.7	932	8	US-11-266-748A-454388
20	447.8	27.6	625	10	US-11-190-172-4076
21	426.8	26.3	430	8	US-11-301-554-1504
22	424	26.2	597	7	US-11-371-354-4921

23	424	25.2	597	7	US-11-371-354-59156
c 24	406.6	25.1	773	7	US-11-344-932-3
c 25	406.6	25.1	773	10	US-11-349-541-3
26	403.2	24.9	793	7	US-11-344-932-33
27	403.2	24.9	793	10	US-11-349-541-33
28	400.2	24.7	816	7	US-11-344-932-2
29	400.2	24.7	816	10	US-11-349-541-2
c 30	275.4	17.0	301	7	US-11-344-932-252
c 31	272.4	16.8	301	7	US-11-344-932-242
c 32	234.8	14.5	5895	6	US-10-527-552-6
33	189.4	11.7	582	8	US-11-266-748A-380888
c 34	189.4	11.7	582	8	US-11-266-748A-464267
c 35	121.4	7.5	1000	8	US-11-266-748A-224722
c 36	121.4	7.5	1000	8	US-11-266-748A-246615
c 37	121.4	7.5	1000	8	US-11-266-748A-398998
c 38	121.4	7.5	1000	8	US-11-266-748A-470044
c 39	104	6.4	676	8	US-11-266-748A-84585
40	104	6.4	676	8	US-11-266-748A-111892
c 41	104	6.4	676	8	US-11-266-748A-137396
c 42	81	5.0	469	10	US-11-292-078-16830
c 43	79.4	4.9	560	10	US-11-292-078-2253
c 44	76.8	4.7	499	10	US-11-292-078-10189
c 45	75.6	4.7	565	10	US-11-292-078-11125

ALIGNMENTS

RESULT 1

US-11-344-932-107
; Sequence 107, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Fa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09

Sequence 59156, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 33, Appl
Sequence 33, Appl
Sequence 2, Appli
Sequence 242, App
Sequence 252, App
Sequence 26615, A
Sequence 398998,
Sequence 470044,
Sequence 84585, A
Sequence 111892,
Sequence 137396,
Sequence 16830, A
Sequence 2253, Ap
Sequence 10189, A
Sequence 11125, A

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-107

Query Match      100.0%; Score 1621; DB 7; Length 1621;
Best Local Similarity 100.0%; Pred. No. 4e-304;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGCACTGCAGGCGATCTGGTCATCGAGCTGTCGGCCCTGGCCCGGCGCGTT 60
Db |||||
Qy 1 CGCCATGCACTGCAGGCGATCTGGTCATCGAGCTGTCGGCCCTGGCCCGGCGCGTT 60
Db |||||

Qy 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCGCGTGTGTAGCGGTGGAACCGCGCGCTC 120
Db |||||

Qy 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCGCGTGTGTAGCGGTGGAACCGCGCGCTC 120
Db |||||

Qy 121 CCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
Db |||||

Qy 121 CCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
Db |||||

Qy 181 GCCCGGGAGCGCGCTGCTGCGGCTGTCGCAAGCGCTCGATGCTGCTGGAGCC 240
Db |||||

Qy 181 GCCCGGGAGCGCGCTGCTGCGGCTGTCGCAAGCGCTCGATGCTGCTGGAGCC 240
Db |||||

Qy 241 CTTCCGCGCGGTGTATGCGAGAACTCCAGTGGGCGCCAGAGATTCCTGACGCGGAAA 300
Db |||||

Qy 301 TCCAAAGGCTTATTTAGCCAGCTGAGTGGATTTGGCCAGCTCAGGAAGCTTCTGCCGTT 360
Db |||||

Qy 301 TCCAAAGGCTTATTTAGCCAGCTGAGTGGATTTGGCCAGCTCAGGAAGCTTCTGCCGTT 360
Db |||||

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTTGCAGAA 420
Db |||||

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTTGCAGAA 420
Db |||||

Qy 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTTAT 480
Db |||||

Qy 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTTAT 480
Db |||||

Qy 481 GTGTGCACTGGGCATTAATAGTCTCTTTTGAACCGCAACGCACTGAAGGCTCAGGT 540
Db |||||

Qy 481 GTGTGCACTGGGCATTAATAGTCTCTTTTGAACCGCAACGCACTGAAGGCTCAGGT 540
Db |||||

Qy 541 CATTGATCCAAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600
Db |||||

Qy 541 CATTGATCCAAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600
Db |||||

Qy 601 GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTATTTGGATGGTGGAGCACCTTT 660
Db |||||

Qy 601 GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTATTTGGATGGTGGAGCACCTTT 660
Db |||||

Qy 661 CTATACGACTTACAGGACAGCACTGAGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
Db |||||

Qy 661 CTATACGACTTACAGGACAGCACTGAGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
Db |||||

Qy 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Db |||||
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RESULT 2

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US-11-349-541-107
; Sequence 107, Application US/11349541
; Publication No. US20060223129A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C7
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Db 721 GTTCTACGAGCTGCTGATCAAGGACTTTGGACTTAAAGTCTGTGTAACCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGATTTTGCAGATGTTATTTGCAAGAGAC 840
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Qy 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGATTTTGCAGATGTTATTTGCAAGAGAC 840
Db |||||

Qy 841 GAAGGCGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCAGAC 900
Db |||||
Qy 841 GAAGGCGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCAGAC 900
Db |||||

Qy 901 TTTTGGAGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTATACACAGTGA 960
Db |||||
Qy 901 TTTTGGAGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTATACACAGTGA 960
Db |||||

Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCCGACCTCCCTTC 1020
Db |||||
Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCCGACCTCCCTTC 1020
Db |||||

Qy 1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACTTCAAGAAATTTGGATT 1080
Db |||||
Qy 1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACTTCAAGAAATTTGGATT 1080
Db |||||

Qy 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAAATAGGTAAA 1140
Db |||||
Qy 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAAATAGGTAAA 1140
Db |||||

Qy 1141 AGTAGTCTCTAACTCCAGGCCCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
Db |||||
Qy 1141 AGTAGTCTCTAACTCCAGGCCCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
Db |||||

Qy 1201 TAGAGTAAACATACAACTTGTATGATGGAACATGAGGAAACAGATTTACAGTGTCTTA 1260
Db |||||
Qy 1201 TAGAGTAAACATACAACTTGTATGATGGAACATGAGGAAACAGATTTACAGTGTCTTA 1260
Db |||||

Qy 1261 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAATTTCAAA 1320
Db |||||
Qy 1261 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAATTTCAAA 1320
Db |||||

Qy 1321 AATGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATGGT 1380
Db |||||
Qy 1321 AATGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATGGT 1380
Db |||||

Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTTATA 1440
Db |||||
Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTTATA 1440
Db |||||

Qy 1441 TTTTGAATGGGTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db |||||
Qy 1441 TTTTGAATGGGTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db |||||

Qy 1501 ATTTACATCTCTGATTTCTCAATGTAGAAAATGAGGAAATGCCCAAAATTTGATGGTGAT 1560
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Qy 1501 ATTTACATCTCTGATTTCTCAATGTAGAAAATGAGGAAATGCCCAAAATTTGATGGTGAT 1560
Db |||||

Qy 1561 AAAAGTCAAGTGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1620
Db |||||
Qy 1561 AAAAGTCAAGTGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1620
Db |||||

Qy 1621 A 1621
Db 1621 A 1621
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US-11-349-541-107
; Sequence 107, Application US/11349541
; Publication No. US20060223129A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C7
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CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT FILING DATE: 2006-02-06
PRIOR APPLICATION NUMBER: US 09/116,134
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,606
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: US 09/020,747
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/806,596
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
TYPE: DNA
ORGANISM: Homo sapien
US-11-349-541-107

Query Match 100.0%; Score 1621; DB 10; Length 1621;
Best Local Similarity 100.0%; Pred. No. 4e-304;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTCGAGGCACTCTCGGTCTATGGAGCTGTCCGGCTGGCCCGCGGCCGCTT 60
DB 1 CGCCATGGCACTCGAGGCACTCTCGGTCTATGGAGCTGTCCGGCTGGCCCGCGGCCGCTT 60

QY 61 CTGTGCTATGTCCTGGCTGACTTTCGGGCGCGTGTGGTACGCTGGACCGGCCGCGCTC 120
DB 61 CTGTGCTATGTCCTGGCTGACTTTCGGGCGCGTGTGGTACGCTGGACCGGCCGCGCTC 120

QY 121 CGCTACGACGTGAGCGCTTGGCGCGGCGGCAAGCGCTCGCTAGTGTGGAAGCTGAGCA 180
DB 121 CGCTACGACGTGAGCGCTTGGCGCGGCGGCAAGCGCTCGCTAGTGTGGAAGCTGAGCA 180

QY 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCC 240
DB 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCC 240

QY 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGAAA 300
DB 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGAAA 300

QY 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAGCTTTCGCGGTT 360
DB 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAGCTTTCGCGGTT 360

QY 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCAAAAATTTGGCAGAG 420
DB 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCAAAAATTTGGCAGAG 420

QY 421 TGGTGAGAAATCCGTATGCCCCCTGAATCTCTGCGCTGACTTTGCTGGTGGCTTAT 480
DB 421 TGGTGAGAAATCCGTATGCCCCCTGAATCTCTGCGCTGACTTTGCTGGTGGCTTAT 480

QY 481 GTGTGACGTGGGATTTAATGGCTCTTTTTCACCGCACACGCTGACAGGGTCAGT 540
DB 481 GTGTGACGTGGGATTTAATGGCTCTTTTTCACCGCACACGCTGACAGGGTCAGT 540

QY 541 CATTTGATGCAAAATATGGTGGAGGACACGATATTTAAGTCTTTTCTGTGGAAGCTCA 600
DB 541 CATTTGATGCAAAATATGGTGGAGGACACGATATTTAAGTCTTTTCTGTGGAAGCTCA 600

QY 601 GAAATCGAGTCTGTGGGAGGACCTTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660
DB 601 GAAATCGAGTCTGTGGGAGGACCTTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660

QY 661 CTATAGCACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGGGCAATAGACCCCA 720
DB 661 CTATAGCACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGGGCAATAGACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGAT 780

DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGAT 780

QY 781 GAGCATGATGATTCGCCAGAAATCAAGAAGTTTTCAGATGATTTTTCGAAAGAAC 840

DB 781 GAGCATGATGATTCGCCAGAAATCAAGAAGTTTTCAGATGATTTTTCGAAAGAAC 840

QY 841 GAAAGCAGATGCTGCTCAAAATCTTTGACGGCACAGATGCTGCTGACCTCCGGTTCGAC 900

DB 841 GAAAGCAGATGCTGCTCAAAATCTTTGACGGCACAGATGCTGCTGACCTCCGGTTCGAC 900

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DB 961 GGAGCAGACGTGAGCGCCCGCCCTGCACTCTGCTGTAAACACCCAGCCATCCCTTC 1020

QY 1021 TTTCAAAAGGGATCCCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080

DB 1021 TTTCAAAAGGGATCCCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080

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DB 1081 CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTAAATAGGATAA 1140

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QY 1261 CCACCTCTAATCAAGAAAGAAATTAAGACTCTGATTTTACAGTGTGATTTGAATTTCTAAA 1320

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QY 1381 AGTTATCTGCTTCCAGTTTGTGATATTTTGTGATATTAAGATTTCTTGAATTTATAT 1440

DB 1381 AGTTATCTGCTTCCAGTTTGTGATATTTTGTGATATTAAGATTTCTTGAATTTATAT 1440

QY 1441 TTTTGAATGGGTTCTAGTGAAGAAATGATATTTCTTGAAGACATCGATATACATTT 1500

DB 1441 TTTTGAATGGGTTCTAGTGAAGAAATGATATTTCTTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTCTTGAATTTACAAATGAGAAATGAGAAATGCCAAATTTGATGTTGAT 1560

DB 1501 ATTTACACTCTTGAATTTACAAATGAGAAATGAGAAATGCCAAATTTGATGTTGAT 1560

QY 1561 AAAAGTCACTGACAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

DB 1561 AAAAGTCACTGACAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

QY 1621 A 1621

DB 1621 A 1621

RESULT 3

US-11-266-748A-23190
; Sequence 23190, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and

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; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55615-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23190
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-23190

Query Match      97.1%; Score 1574.2; DB 8; Length 2005;
Best Local Similarity 99.8%; Pred. No. 4.7e-295;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1  CGCCATGGCACTGCAGGGCACTCTGGTCAATGGAGCTGTCCGGCTTGGCCCGCCCGGCGCGTT 60
Db 62  CGCCATGGCACTGCAGGGCACTCTGGTCTGTGGAGCTGTCCGGCTTGGCCCGCCCGGCGCGTT 121

Qy 61  CTGTGCTATGCTCTGGTCTGAGCTTCCGGGGCGGTGTGTAGCGTGGACCGCGCGGCTC 120
Db 122  CTGTGCTATGCTCTGGTCTGAGCTTCCGGGGCGGTGTGTAGCGTGGACCGCGCGGCTC 181

Qy 121  CGGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGGACCTGGAAGCA 180
Db 182  CGGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGGACCTGGAAGCA 241

Qy 181  GCCCGGGAGCCGCGCTGCTCGCGCTGTGTGCAAGCGGTCCGATGCTGCTGGAGCC 240
Db 242  GCCCGGGAGCCGCGCTGCTCGCGCTGTGTGCAAGCGGTCCGATGCTGCTGGAGCC 301

Qy 241  CTTCCGCGCGGTGTCAATGGAGAACTCCAGTGGGCGCCAGAGATTCTGACGCGGAA 300
Db 302  CTTCCGCGCGGTGTCAATGGAGAACTCCAGTGGGCGCCAGAGATTCTGACGCGGAA 361

Qy 301  TCCAAAGGCTTATTTATGCGAGCTCAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
Db 362  TCCAAAGGCTTATTTATGCGAGCTCAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTT 421

Qy 361  AGCTGGCCACGATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 420
Db 422  AGCTGGCCACGATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 481

Qy 421  TGGTGAGAAATCGGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGTGGCTTAT 480
Db 482  TGGTGAGAAATCGGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGTGGCTTAT 541

Qy 481  GTGTGCACTGGGCATTATAAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGTCAGGT 540
Db 542  GTGTGCACTGGGCATTATAAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGTCAGGT 601

Qy 541  CATTTGATCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTCTGTGGAACCTCA 600
Db 602  CATTTGATCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTCTGTGGAACCTCA 661

Qy 601  GAAATCGAGTCTGTGGGAGACCTCGAGGACAGAACTGTGGATGTGGAGCACCTTT 660
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RESULT 4

US-11-343-797-104

; Sequence 104, Application US/11343797

; Publication No. US20060211017A1

; GENERAL INFORMATION:

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Db 662  GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTGGATGGTGAGCACTTT 721
Qy 661  CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 722  CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 781
Qy 721  GTTCTACGAGCTGCTGATCAAGGACTTGGAGCTTAAAGTCTGATGAATCCCAATCAGAT 780
Db 782  GTTCTACGAGCTGCTGATCAAGGACTTGGAGCTTAAAGTCTGATGAATCCCAATCAGAT 841
Qy 781  GAGCATGATGATTGGCCAGAAATGAAGAAAGTGTTCAGATGATATTTCGAAAGAAAGAC 840
Db 842  GAGCATGATGATTGGCCAGAAATGAAGAAAGTGTTCAGATGATATTTCGAAAGAAAGAC 901
Qy 841  GAAAGGACAGAGTGTCTCAAAATCTTTTGACGGCACAGATGCTGTGTGATCTCCGGTTCGAC 900
Db 902  GAAAGGACAGAGTGTCTCAAAATCTTTTGACGGCACAGATGCTGTGTGATCTCCGGTTCGAC 961
Qy 901  TTTTGAGGAGGTGTTTCATCATGATCAACACAGGACGGGCTCGTTTATCACCAGTGA 960
Db 962  TTTTGAGGAGGTGTTTCATCATGATCAACACAGGACGGGCTCGTTTATCACCAGTGA 1021
Qy 961  GGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTAAACACACCCAGCCATCCCTTC 1020
Db 1022  GGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTAAACACACCCAGCCATCCCTTC 1081
Qy 1021  TTTCAAAAAGGATCTCTTTTCATAGAGAAACACATCGAGGAGATCTTGAAGAAATTTGAT 1080
Db 1082  TTTCAAAAAGGATCTCTTTTCATAGAGAAACACATCGAGGAGATCTTGAAGAAATTTGAT 1141
Qy 1081  CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Db 1142  CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1201
Qy 1141  AGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATATCTGCAATTTACAGTG 1200
Db 1202  AGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATATCTGCAATTTACAGTG 1261
Qy 1201  TAGAGTAACACATAACTATGATGATGCAATGGAAACATGAGGAAACAGTATTACAGTGTCTA 1260
Db 1262  TAGAGTAACACATAACTATGATGATGCAATGGAAACATGAGGAAACAGTATTACAGTGTCTA 1321
Qy 1261  CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTCAATGATTAATCTAAA 1320
Db 1322  CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTCAATGATTAATCTAAA 1381
Qy 1321  AATGGTTATCAATAGGCGCTTTTGATTTTATAAACTTTGGGTACTTATACTATAAATATGTT 1380
Db 1382  AATGGTTATCAATAGGCGCTTTTGATTTTATAAACTTTGGGTACTTATACTATAAATATGTT 1441
Qy 1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTTGATATATA 1440
Db 1442  AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTTGATATATA 1501
Qy 1441  TTTTGAATGGTCTTAGTGAAGAAAGATGATATTTCTTGAACACATCGATATACATTT 1500
Db 1502  TTTTGAATGGTCTTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1561
Qy 1501  ATTTTACACTCTTGATTTCTACAAATCTAGAAATAGGAAATGCCACAAATTTATATGTTGAT 1560
Db 1562  ATTTTACACTCTTGATTTCTACAAATCTAGAAATAGGAAATGCCACAAATTTATATGTTGAT 1621
Qy 1561  AAAAGTCACGTGAAACAAA 1579
Db 1622  AAAAGTCACGTGAAACAGA 1640
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APPLICANT: Chinmaiyan, Arul M.
APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/11/343,797
CURRENT FILING DATE: 2006-01-31
PRIORITY APPLICATION NUMBER: US/10/210,120
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: US 60/309,581
PRIORITY FILING DATE: 2001-08-02
PRIORITY APPLICATION NUMBER: US 60/334,468
PRIORITY FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn version 3.2
SEQ ID NO 104
LENGTH: 2005
TYPE: DNA
ORGANISM: Homo sapiens
US-11-343-797-104

Query Match 97.1%; Score 1574.2; DB 10; Length 2005;
Best Local Similarity 99.8%; Pred. No. 4.7e-295;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCGGGCTCGGCCCGCGGCCCGTT	60
DB	62	CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCGGGCTCGGCCCGCGGCCCGTT	121
QY	61	CTGTGCTATGGTCTCGGCTGACTTCGGGCGCGGTGTGGTACGCGTGGACCGGCGCGGCTC	120
DB	122	CTGTGCTATGGTCTCGGCTGACTTCGGGCGCGGTGTGGTACGCGTGGACCGGCGCGGCTC	181
QY	121	CGCTACGACGTGAGCGGCTTGGGCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCA	180
DB	182	CGCTACGACGTGAGCGGCTTGGGCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCA	241
QY	181	GCGCGGGGAGCGCGGCTGTCGGGCGGTCTGTGCAAGCGGTGGATGTCGTGGAGCC	240
DB	242	GCGCGGGGAGCGCGGCTGTCGGGCGGTCTGTGCAAGCGGTGGATGTCGTGGAGCC	301
QY	241	CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGACGGGAAA	300
DB	302	CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGACGGGAAA	361
QY	301	TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTACGGAAGCTTCTGCCGTT	360
DB	362	TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTACGGAAGCTTCTGCCGTT	421
QY	361	AGTGGCCACGATATCAACTATTTGGCTTTGTGAGGCTTCTCTCAAAATTTGGCAGAAG	420
DB	422	AGTGGCCACGATATCAACTATTTGGCTTTGTGAGGCTTCTCTCAAAATTTGGCAGAAG	481
QY	421	TGGTGAATTCGGTATGCCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTAT	480
DB	482	TGGTGAATTCGGTATGCCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTAT	541
QY	481	GTGTGACCTGGGATTTATATGGCTCTTTTGGACCGCACCGCATGCAAGGGTCAGGT	540
DB	542	GTGTGACCTGGGATTTATATGGCTCTTTTGGACCGCACCGCATGCAAGGGTCAGGT	601
QY	541	CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTCTTTTCTGTGGAACTCA	600
DB	602	CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTCTTTTCTGTGGAACTCA	661
QY	601	GAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT	660
DB	662	GAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT	721
QY	661	CTATACGACTTACGAGACAGCATGGGAAATTCATGGCTGTGTGGAGCAATGAACCCCA	720
DB	722	CTATACGACTTACGAGACAGCATGGGAAATTCATGGCTGTGTGGAGCAATGAACCCCA	781

QY	721	GTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACATTTCCCAATCAGAT	780
DB	782	GTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACATTTCCCAATCAGAT	841
QY	781	GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTGCAAGAGAC	840
DB	842	GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTGCAAGAGAC	901
QY	841	GAAGCAGAGTGTGTCAAACTTTTGACGGCAGAGTCTGTGTGACTCCGGTTCCTGAC	900
DB	902	GAAGCAGAGTGTGTCAAACTTTTGACGGCAGAGTCTGTGTGACTCCGGTTCCTGAC	961
QY	901	TTTTGAGGAGTGTTCATCATGATCACAACAAAGGAACGGGCTCGTTTATCACCACTGA	960
DB	962	TTTTGAGGAGTGTTCATCATGATCACAACAAAGGAACGGGCTCGTTTATCACCACTGA	1021
QY	961	GGAGCAGGAGTGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC	1020
DB	1022	GGAGCAGGAGTGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC	1081
QY	1021	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT	1080
DB	1082	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT	1141
QY	1081	CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAA	1140
DB	1142	CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAA	1201
QY	1141	AGCTAGTCTTAACCTTCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG	1200
DB	1202	AGCTAGTCTTAACCTTCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG	1261
QY	1201	TAGAGTAAACATTAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1260
DB	1262	TAGAGTAAACATTAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1321
QY	1261	CCACTCTAATCAAGAAAAGATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA	1320
DB	1322	CCACTCTAATCAAGAAAAGATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA	1381
QY	1321	AATGGTATCATAGGGCTTTTGAATTTAATAAACTTTGGGTACTTATTAATTAATTTGGT	1380
DB	1382	AATGGTATCATAGGGCTTTTGAATTTAATAAACTTTGGGTACTTATTAATTAATTTGGT	1441
QY	1381	AGTTATCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA	1440
DB	1442	AGTTATCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA	1501
QY	1441	TTTTGAATGGGTCTAGTGAAGAAAGATGATATATTTTGAAGACATCGATATACATTT	1500
DB	1502	TTTTGAATGGGTCTAGTGAAGAAAGATGATATATTTTGAAGACATCGATATACATTT	1561
QY	1501	ATTTACACTTTGATTTCAATGTAGAAAATGAGAAAATGCCAATAATTTGATGTTGAT	1560
DB	1562	ATTTACACTTTGATTTCAATGTAGAAAATGAGAAAATGCCAATAATTTGATGTTGAT	1621
QY	1561	AAAGCTCAGTGAAACABA 1579	
DB	1622	AAAGCTCAGTGAAACABA 1640	

RESULT 5
US-11-266-748A-22797
; Sequence 22797, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A

;; CURRENT FILING DATE: 2005-11-03
;; PRIOR APPLICATION NUMBER: EP 04105479.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105482.6
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105483.4
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105507.0
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105485.9
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105484.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: US 60/662,276
;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700,293
;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 22797
;; LENGTH: 2041
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-11-266-748A-22797

Query Match 96.9%; Score 1571; DB 8; Length 2041;

Best Local Similarity 99.7%; Pred. No. 2e-294;
Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	CGCCATGCGCATCGAGGCGATCTCGGTCTATGGAGTGTCCGGCTCGGCCCGCGGCCCGTT	60
Db	85	CGCCATGCGCATCGAGGCGATCTCGGTCTATGGAGTGTCCGGCTCGGCCCGCGGCCCGTT	144
Qy	61	CTGTGCTATGTCCTGCGTGTGCTGCGGCGCGTGTGCTGACGCGTGGACCGCGCCGCTC	120
Db	145	CTGTGCTATGTCCTGCGTGTGCTGCGGCGCGTGTGCTGACGCGTGGACCGCGCCGCTC	204
Qy	121	CGGTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGGTCTGCGTGGACCTGAAGCA	180
Db	205	CGGTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGGTCTGCGTGGACCTGAAGCA	264
Qy	181	GCCGCGGGAGCGCGCTGCGCGCTGTGCAAGCGTGTGCAAGCGTGTGCTGGAGCC	240
Db	265	GCCGCGGGAGCGCGCTGCGCGCTGTGCAAGCGTGTGCAAGCGTGTGCTGGAGCC	324
Qy	241	CTTCGCGCGCGTGTGTCAGGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAA	300
Db	325	CTTCGCGCGCGTGTGTCAGGAACTCCAGCTGGGCCAGAGATTTCTGACGCGGAAA	384
Qy	301	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360
Db	385	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	444
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAG	420
Db	445	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAG	504
Qy	421	TGGTGAGAAATCCGATATGCGCGCTGAATCTCTGCGTCACTTTGCTGGTGGCTTTAT	480
Db	505	TGGTGAGAAATCCGATATGCGCGCTGAATCTCTGCGTCACTTTGCTGGTGGCTTTAT	564
Qy	481	GTGTGCACTGGGCATTAATAGTCTTTTGGACCGGACAGCACTGACAGGGTCAGGT	540
Db	565	GTGTGCACTGGGCATTAATAGTCTTTTGGACCGGACAGCACTGACAGGGTCAGGT	624
Qy	541	CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGGAACCTCA	600
Db	625	CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGGAACCTCA	684
Qy	601	GAATTCGAGTCTGTGGGAGGACCTTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTT	660
Db	685	GAATTCGAGTCTGTGGGAGGACCTTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTT	744

RESULT 6
US-11-266-748A-23899
; Sequence 23899, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl

Qy	661	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCCA	720
Db	745	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCCA	804
Qy	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT	780
Db	805	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT	864
Qy	781	GAGCATGGATGATGGCCGAAATGAGAGAAATTTGCAGATGATTTGCAAGAGAGAC	840
Db	865	GAGCATGGATGATGGCCGAAATGAGAGAAATTTGCAGATGATTTGCAAGAGAGAC	924
Qy	841	GAAGGACAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGTGACTCCGGTCTTGAC	900
Db	925	GAAGGACAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGTGACTCCGGTCTTGAC	984
Qy	901	TTTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA	960
Db	985	TTTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA	1044
Qy	961	GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTAAACACCCCGACCATCCCTTC	1020
Db	1045	GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTAAACACCCCGACCATCCCTTC	1104
Qy	1021	TTTCAAAAGGATCTCTTTCATAGAGAAACACATGAGGAGATCTTGAAGAATTTGGATT	1080
Db	1105	TTTCAAAAGGATCTCTTTCATAGAGAAACACATGAGGAGATCTTGAAGAATTTGGATT	1164
Qy	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATAGGTAAA	1140
Db	1165	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATAGGTAAA	1224
Qy	1141	AGCTAGTCTCTTAACCTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1200
Db	1225	AGCTAGTCTCTTAACCTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1284
Qy	1201	TAGAGTAAACATAACTATGTCATGCAAGAAACATGGAGAAACAGTATTTACAGTGTCTTA	1260
Db	1285	TAGAGTAAACATAACTATGTCATGCAAGAAACATGGAGAAACAGTATTTACAGTGTCTTA	1344
Qy	1261	CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATCTACAGTGAATGAATTTCTAAA	1320
Db	1345	CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATCTACAGTGAATGAATTTCTAAA	1404
Qy	1321	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGCTACTTATACTAAATATGTT	1380
Db	1405	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGCTACTTATACTAAATATGTT	1464
Qy	1381	AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTTCTTGACTTATA	1440
Db	1465	AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTTCTTGACTTATA	1524
Qy	1441	TTTTGAATGGGTTCTAGTGAAAAGGAATGATATTTCTTTGAAGACATTCGATATACATTT	1500
Db	1525	TTTTGAATGGGTTCTAGTGAAAAGGAATGATATTTCTTTGAAGACATTCGATATACATTT	1584
Qy	1501	ATTTACACTCTTGATTTCTACAAATGAGGAAATGAGGAAATGCCCAAAATTTGATGTTGAT	1560
Db	1585	ATTTACACTCTTGATTTCTACAAATGAGGAAATGAGGAAATGCCCAAAATTTGATGTTGAT	1644
Qy	1561	AAAGTCCAGTGAACAAA 1579	
Db	1645	AAAGTCCAGTGAACAAA 1663	

;; TITLE OF INVENTION: Transcriptome Microarray Technology and

;; FILE REFERENCE: 55815-0102 (319189)

;; CURRENT APPLICATION NUMBER: US/11/266,748A

;; CURRENT FILING DATE: 2005-11-03

;; PRIOR APPLICATION NUMBER: EP 04105479.2

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: EP 04105482.6

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: EP 04105483.4

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: EP 04105507.0

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: EP 04105485.9

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: EP 04105484.2

;; PRIOR FILING DATE: 2004-11-03

;; PRIOR APPLICATION NUMBER: US 60/662,276

;; PRIOR FILING DATE: 2005-03-14

;; PRIOR APPLICATION NUMBER: US 60/700,293

;; PRIOR FILING DATE: 2005-07-18

;; NUMBER OF SEQ ID NOS: 483996

;; SOFTWARE: Patent in version 3.3

;; SEQ ID NO 23899

;; LENGTH: 2068

;; TYPE: DNA

;; ORGANISM: Homo Sapiens

;; FEATURE:

;; NAME/KEY: misc.feature

;; LOCATION: (143)..(143)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-23899

Query Match 94.1%; Score 1524.8; DB 8; Length 2068;

Best Local Similarity 98.6%; Pred. No. 1.7e-285;

Matches 1559; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

Qy	1	CGCCATGGCAGTGGGCGATCTCGTCAATGAGCTGTCGGGCGCTGGGCGCGGCGGCTT	60
Db	85	CGCCATGGCAGTGGGCGATCTCGTCAATGAGCTGTCGGGCGCTGGGCGCGGCGGCTT	144
Qy	61	CTGTGCTATGTCCTGGCTGACTTCGGGCGGCGTGTGTACGCTGGGCGGCGGCTC	120
Db	145	CTGTGCTATGTCCTGGCTGACTTCGGGCGGCGTGTGTACGCTGGGCGGCGGCTC	204
Qy	121	CGGCTACGAGCTGAGCGGCTTGGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG	180
Db	205	CGGCTACGAGCTGAGCGGCTTGGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG	264
Qy	181	CGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
Db	265	CGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	322
Qy	241	CTTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
Db	323	CTTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	382
Qy	301	TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGT--CAGGAAGCTTCTG	358
Db	383	TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGT--CAGGAAGCTTCTG	442
Qy	359	TTAGTGGCGCAGATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGG	418
Db	443	TTAGTGGCGCAGATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGG	502
Qy	419	AGTGGTGAGAACTCCGCTATGCCCGCTGAATCTCTGGCTGCTGCTGCTGCTG	478
Db	503	AGTGGTGAGAACTCCGCTATGCCCGCTGAATCTCTGGCTGCTGCTGCTGCTG	562
Qy	479	ATGTGTGCACTGGGCAATTAATAGCTCTTTTGGACCGCACACGCACTGACAGG	538
Db	563	ATGTGTGCACTGGGCAATTAATAGCTCTTTTGGACCGCACACGCACTGACAGG	622

RESULT 7

US-11-266-748A-57286
; Sequence 57286, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57286
; LENGTH: 2373
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-57286

Query Match 76.5%; Score 1240.6; DB 8; Length 2373;
Best Local Similarity 89.6%; Pred. No. 1.6e-230;
Matches 1414; Conservative 0; Mismatches 4; Indels 161; Gaps 1;

Qy	1	CGCCATGCGCATCTGAGGCGCATCTCGGTCTATCGAGCTGTCGGGCTGGCCCGGCGCCGTT	60
Db	79	CGCCATGCGCATCTGAGGCGCATCTCGGTCTGAGCTGTCGGGCTGGCCCGGCGCCGTT	138
Qy	61	CTGTGCTATGTCCTGCTGACTTTGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTC	120
Db	139	CTGTGCTATGTCCTGCTGACTTTGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTC	198
Qy	121	CCGCTACGACGTGAGCGCGTTGGGCGGGGCAAGCGCTCGGTAGTCTGGACCTGAAGCA	180
Db	199	CCGCTACGACGTGAGCGCGTTGGGCGGGGCAAGCGCTCGGTAGTCTGGACCTGAAGCA	258
Qy	181	GCCGCGGGAGCGCGGTCGCGCGCTGTGCAAGCGGTGCGATGTCGCTGGAGCC	240
Db	259	GCCGCGGGAGCGCGGTCGCGCGCTGTGCAAGCGGTGCGATGTCGCTGGAGCC	318
Qy	241	CTTCCGCGCGGTGTCTATGCGAAGAACTCCAGCTGGGCGCCAGAGATTTCTGACGCGGAAA	300
Db	319	CTTCCGCGCGGTGTCTATGCGAAGAACTCCAGCTGGGCGCCAGAGATTTCTGACGCGGAAA	378
Qy	301	TCCAAGGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGGAGCTTCTGCCGTT	360
Db	379	TCCAAGGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGGAGCTTCTGCCGTT	438
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTCTGTCAGGTGTTCTCAAAAATTGGCAGAAG	420
Db	439	AGCTGGCCACGATATCAACTATTTGGCTTCTGTCAGGTGTTCTCAAAAATTGGCAGAAG	472
Qy	421	TGGTGAGAAATCCGTATGCGCGCTGAAATCTCTCGGCTGACTTTGCTGGTGGTGGCTTAT	480
Db	473	-----	472

Qy	481	GTGTGCACTGGGCATTATATGCTCTTTTGTGACCGCACACGCACTGACAAAGGTCAGGT	540
Db	473	-----	472
Qy	541	CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTCTTTTCTGTGGAATACTCA	600
Db	473	-----GTTGGAAGGAAACAGCATATTTAAGTCTTTTCTGTGGAATACTCA	517
Qy	601	GAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT	660
Db	518	GAATTTGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT	577
Qy	661	CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720
Db	578	CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	637
Qy	721	GTTCTACGAGCTGCTGATCAAGGAACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT	780
Db	638	GTTCTACGAGCTGCTGATCAAGGAACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT	697
Qy	781	GAGCATGGATGATGGCCAGAAATGAGAAAGATTTGCAAGATGCTATTTCCAAAGAGAC	840
Db	698	GAGCATGGATGATGGCCAGAAATGAGAAAGATTTGCAAGATGCTATTTCCAAAGAGAC	757
Qy	841	GAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC	900
Db	758	GAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC	817
Qy	901	TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA	960
Db	818	TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA	877
Qy	961	GGAGGAGGACGTGAGCGCCCGCCCTGCACTCTGCTGTTAAACACCCCGACCATCCCTTC	1020
Db	878	GGAGGAGGACGTGAGCGCCCGCCCTGCACTCTGCTGTTAAACACCCCGACCATCCCTTC	937
Qy	1021	TTTCAAAAGGATCTTTTCATAGGAGAAACACACTGAGGAGATACTCTCAAGAATTTGAGTT	1080
Db	938	TTTCAAAAGGATCTTTTCATAGGAGAAACACACTGAGGAGATACTCTGAGAGATTTGAGTT	997
Qy	1081	CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1140
Db	998	CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1057
Qy	1141	AGCTAGTCTCTAACTTCAGGCCCAAGCGCTCAAGTGAATTTGATATGCAATTTACAGTG	1200
Db	1058	AGCTAGTCTCTAACTTCAGGCCCAAGCGCTCAAGTGAATTTGATATGCAATTTACAGTG	1117
Qy	1201	TAGAGTAACACATAAATGTTGTCATGGAACACATGGAGAAACAGATATTACAGTGTCTTA	1260
Db	1118	TAGAGTAACACATAAATGTTGTCATGGAACACATGGAGAAACAGATATTACAGTGTCTTA	1177
Qy	1261	CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTACAGTGATGATTAATTTCTAAA	1320
Db	1178	CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTACAGTGATGATTAATTTCTAAA	1237
Qy	1321	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTACTATAAATATGTT	1380
Db	1238	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTACTATAAATATGTT	1297
Qy	1381	AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTATA	1440
Db	1298	AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTATA	1357
Qy	1441	TTTTGAAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTTGAAGACATCGATATACATTT	1500
Db	1358	TTTTGAAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTTGAAGACATCGATATACATTT	1417
Qy	1501	ATTTACACTCTGTTGATTTCTACAAATGAGAAATGAGGAAATGCCACAAATTTGTATGTTGAT	1560
Db	1418	ATTTACACTCTGTTGATTTCTACAAATGAGGAAATGAGGAAATGCCACAAATTTGTATGGTGTAT	1477
Qy	1561	AAAAGTCACGTGAACAAA	1579

Db 1478 AAAAGTCAAGTGAACAGAGA 1496
|||||
1032 TGCTGATCAAGGACTTGAGCTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATG 791
|||||
807 TGCTGATCAAGGACTTGAGCTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATG 748
|||||
792 ATTGGCCAGAAATGAAGAAAGAGTTTGCAGATGTTTGCAGATGTTTGCAGATGAGCATGAGCATG 851
|||||
747 ATTGGCCAGAAATGAAGAAAGAGTTTGCAGATGTTTGCAGATGTTTGCAGATGAGCATGAGCATG 688
|||||
852 GGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTTGACTCTTTTGAGGAGG 911
|||||
687 GGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTTGACTCTTTTGAGGAGG 628
|||||
912 TTGTTTCATCATGATCACAACAGGAAACGGGGCTCGTTTATCACCAGTGAAGGAGGAGGAGG 971
|||||
627 TTGTTTCATCATGATCACAACAGGAAACGGGGCTCGTTTATCACCAGTGAAGGAGGAGGAGG 568
|||||
972 TGAGCCCGCCGCTGACCTCTGCTGTGTTAAACACCCAGCCATCCCTCTTTTCAAAGGG 1031
|||||
567 TGAGCCCGCCGCTGACCTCTGCTGTGTTAAACACCCAGCCATCCCTCTTTTCAAAGGG 508
|||||
1032 ATCTCTTTTCATGAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGCGGGAAG 1091
|||||
507 ATCTCTTTTCATGAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGCGGGAAG 448
|||||
1092 AGATTTCATGAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGCGGGAAG 1151
|||||
447 AGATTTCATGAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATTTCAGCGGGAAG 388
|||||
1152 AACTTCCAGGCCCAGGCTCAAGTGAATTTGAAATCTGCAATTCAGTGTAGAGTAACAC 1211
|||||
387 AACTTCCAGGCCCAGGCTCAAGTGAATTTGAAATCTGCAATTCAGTGTAGAGTAACAC 328
|||||
1212 ATACATTTGTATGATGGAACATCGAGGAGAACAGTATTACAGTGTCCCTACCACTCTAATC 1271
|||||
327 ATACATTTGTATGATGGAACATCGAGGAGAACAGTATTACAGTGTCCCTACCACTCTAATC 268
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1272 AAGAAAAGAAATTCACAGACTCTGATTCTACAGTGTGATGAAATTTCTAAAAATGGTTATCA 1331
|||||
267 AAGAAAAGAAATTCACAGACTCTGATTCTACAGTGTGATGAAATTTCTAAAAATGGTTATCA 208
|||||
1332 TTAGGGCTTTTGAATTTATAAAACTTTGGGTACTTATATCTAAATTTATGGTATTTCTGCG 1391
|||||
207 TTAGGGCTTTTGAATTTATAAAACTTTGGGTACTTATATCTAAATTTATGGTATTTCTGCG 148
|||||
1392 CTTCCAGTTTCTGATATATTTGTTGATTTAAAGATTTCTGATTTATTTTGAATGGG 1451
|||||
147 CTTCCAGTTTCTGATATATTTGTTGATTTAAAGATTTCTGATTTATTTTGAATGGG 88
|||||
1452 TTCTAGTGAAGAAAGGATGATATATTTCTTGAAGACATCGATATACATTTATTTTACACTCT 1511
|||||
87 TTCTAGTGAAGAAAGGATGATATATTTCTTGAAGACATCGATATACATTTATTTTACACTCT 28
|||||
1512 TGATTTCTCAATGTGAGAAATGAGGAA 1538
|||||
27 NGANNCTCAATGTAGAAAAGCGGAAA 1
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RESULT 9

US-11-266-748A-237887
; Sequence 237887, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6

Db 1478 AAAAGTCAAGTGAACAGAGA 1496
|||||
612 TGTGGAAGCACCCTCGAGGACAGAACATGTTGATGGTGGAGCACCCTTTCTATACACTT 671
|||||
926 YGTGTGGAACMCTTCGMAACAGGACATGKTGNTGTT-GRGACCTTTTCWAWACACTA 868
|||||
672 ACAGGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGC 731
|||||
867 ACAGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGC 808
|||||

Query Match 54.4%; Score 882.2; DB 8; Length 971;
Best Local Similarity 96.3%; Pred. No. 2.4e-161;
Matches 893; Conservative 10; Mismatches 23; Indels 1; Gaps 1;
Query 612 TGTGGAAGCACCCTCGAGGACAGAACATGTTGATGGTGGAGCACCCTTTCTATACACTT 671
Db 926 YGTGTGGAACMCTTCGMAACAGGACATGKTGNTGTT-GRGACCTTTTCWAWACACTA 868
Query 672 ACAGGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGC 731
Db 867 ACAGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGC 808
|||||

US-11-266-748A-215905
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (23)..(24)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (27)..(27)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (35)..(36)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (39)..(39)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (893)..(893)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-215905

[illegible]

; NAME/KEY: misc.feature
; LOCATION: (709)..(709)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-46436

Query Match 48.3%; Score 783; DB 8; Length 958;
Best Local Similarity 95.8%; Pred. No. 3.7e-142;
Matches 858; Conservative 0; Mismatches 31; Indels 7; Gaps 5;

QY 675 GGACACGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 734
DB |||||||
QY 12 GGACACGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 70
DB |||||||
QY 735 TGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGACATGGATGAT 794
DB |||||||
QY 71 TGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGACATGGATGAT 130
DB |||||||
QY 795 GGCCAGAAATGAAGAAGATTTGACAGATGATTTGCAAGAAGACGAAGGACAGATGAT 854
DB |||||||
QY 131 GGCCAGAAATGAAGAAGATTTGACAGATGATTTGCAAGAAGACGAAGGACAGATGAT 190
DB |||||||
QY 855 GTCAATCTTTGACGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 914
DB |||||||
QY 191 GTCAATCTTTGACGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 250
DB |||||||
QY 915 TTCAATCATGATCACAACAGGAAGCGGGCTCGTTTATCACAGTGAAGGACGAGCTGA 974
DB |||||||
QY 251 TTCAATCATGATCACAACAGGAAGCGGGCTCGTTTATCACAGTGAAGGACGAGCTGA 310
DB |||||||
QY 975 GCGCCCGCCCTGCCTCTGTGTTAAACACCCCGCCATCCCTCTTTCAAAGGGATC 1034
DB |||||||
QY 311 GCGCCCGCCCTGCCTCTGTGTTAAACACCCCGCCATCCCTCTTTCAAAGGGATC 370
DB |||||||
QY 1035 CTTTCATAGAGACACACCTGAGGAGATCTTGAAGAAATTTGGATTACGCCCGGAGAGA 1094
DB |||||||
QY 371 CTTTCATAGAGACACACCTGAGGAGATCTTGAAGAAATTTGGATTACGCCCGGAGAGA 430
DB |||||||
QY 1095 TTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAGCTAGTCTCTAAC 1154
DB |||||||
QY 431 TTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAGCTAGTCTCTAAC 490
DB |||||||
QY 1155 TTCCAGGCCACGGCTCAAGTGAATTTGAATAGTCTGATTTACAGTGTAGAGTAACACATA 1214
DB |||||||
QY 491 TTCCAGGCCACGGCTCAAGTGAATTTGAATAGTCTGATTTACAGTGTAGAGTAACACATA 550
DB |||||||
QY 1215 ACATTGTATGATGAGAAACATGAGGAACAGTATTTACAGTGTCTACCACTTAATCAAG 1274
DB |||||||
QY 551 ACATTGTATGATGAGAAACATGAGGAACAGTATTTACAGTGTCTACCACTTAATCAAG 610
DB |||||||
QY 1275 AAAAGAAATTCAGACTCTGATCTTACAGTGAATTTGAATTTCTAAAATGGTTATCATTA 1334
DB |||||||
QY 611 AAAAGAAATTCAGACTCTGATCTTACAGTGAATTTGAATTTCTAAAATGGTTATCATTA 670
DB |||||||
QY 1335 GGGCTTTGATTTATAAAACTTTGGTACTTATA-CTAAATATGTTAGTATTTCTGCT 1393
DB |||||||
QY 671 GGGCTTTGATTTATAAAACTTTGGTACTTATACTTAACTANATTTAGTATTTCTGCT 730
DB |||||||
QY 1394 TCCAGTTTCCTGATATATTTGTTGATATTAAGATTTCTTGAATTTATTTGAAATGGGTT 1453
DB |||||||
QY 731 TCCAGTTTCCTGATATATTTGTTGAAATTTGAATTTCTTGAATTTATTTTTC-ATGGGTT 789
DB |||||||
QY 1454 CTAGTGAAAGGAATGATATATTTCTTGAAGACATGATATACATTTATTTACCTCTTG 1513
DB |||||||
QY 790 CTAGTGAAAGGAATGATATTTATTTCTTGAAGACATGATTTATTTATTTTAACTTTCTTG 849
DB |||||||
QY 1514 ATTCTACAATGTAGAAAT--GAGGAAATGCCACAAATG--TATGGTGATAAAG 1565
DB |||||||
QY 850 ATTTTACAATGTCAAAATTTGAGGAAATGCCCAATTTGGTTATGGTGATATAG 905
DB |||||||

RESULT 11
US-11-266-748A-84584
; Sequence 84584, Application US/11266748A

; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84584
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (773)..(773)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (822)..(822)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (903)..(903)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-84584

Query Match 45.3%; Score 734.6; DB 8; Length 924;
Best Local Similarity 97.7%; Pred. No. 8.3e-133;
Matches 798; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

QY 719 CAGTTCTACGAGCTCTGATCAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAG 778
DB |||||||
QY 1 CAGTTTACGAGCTGTGA-CAAGGCACTGGACTAAAGTCTGATGACCTTCCCAATCAG 59
DB |||||||
QY 779 ATGACATGGATGATGTCGCCAGAAATGAAGAAAGATTTGAGATGATTTGCAAGAAG 838
DB |||||||
QY 60 ATGACATGGATGATTTGGCCAGAAATGAAGAAAGATTTGAGATGATTTGCAAGAAG 119
DB |||||||
QY 839 ACGAGGCGAGTGGTGTCAATCTTTGACCGCACAGATGCTGTGCTGCTCCGTTCTG 898
DB |||||||
QY 120 ACGAAGCGAGTGGTGTCAATCTTTGACCGCACAGATGCTGTGCTGCTCCGTTCTG 179
DB |||||||
QY 899 ACTTTTGAAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGT 958
DB |||||||
QY 180 ACTTTTGAAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGT 239
DB |||||||
QY 959 GAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCT 1018
DB |||||||
QY 240 GAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCT 299
DB |||||||

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Qy 1019 TCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGA 1078
Db 300 TCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGA 359
Qy 1079 TTCAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTA 1138
Db 360 TTCAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTA 419
Qy 1139 AAAGCTAGTCTCTAACTTCCAGGCCACCGGCTC-AAAGTGAATTTGAATACCTGCAATTTACA 1197
Db 420 AAAGCTAGTCTCTAACTTCCAGGCCACCGGCTC-AAAGTGAATTTGAATACCTGCAATTTACA 479
Qy 1198 GTGTAGAGTAACACATAACATTTGATGATGCAATGGAACATGAGGAGAACAGTATTAAGTGT 1257
Db 480 GTGTAGAGTAACACATAACATTTGATGATGCAATGGAACATGAGGAGAACAGTATTAAGTGT 539
Qy 1258 CTACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCT 1317
Db 540 CTACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCT 599
Qy 1318 AAAAATGGTTATCATTTAGGGCTTTTGGATTTATAAACTTTGGGTACTTTATATAAAATTTAT 1377
Db 600 AAAAATGGTTATCATTTAGGGCTTTTGGATTTATAAACTTTGGGTACTTTATATAAAATTTAT 659
Qy 1378 GGTAGTATTCTGCCTCCAGTTTGCCTGATATATTTGTTGATATTAAGATTTCTTGACTT 1437
Db 660 GGTAGTATTCTGCCTCCAGTTTGCCTGATATATTTGTTGATATTAAGATTTCTTGACTT 719
Qy 1438 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATT-CTTGAAGACATC-GATATA 1495
Db 720 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATT-CTTGAAGACATCNGATATA 779
Qy 1496 CATTTATTTACACTCTT-GATTCTACAATGTAGAAA 1531
Db 780 CATTTATTTACACTCTTGGATTTCAATGGTAGAAA 816
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RESULT 12

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US-11-266-748A-111891
; Sequence 111891, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111891
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo Sapiens
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Query Match 45.3%; Score 734.6; DB 8; Length 924;
Best Local Similarity 97.7%; Pred. No. 8.3e-133; Indels 5; Gaps 5;
Matches 798; Conservative 0; Mismatches 14;

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Qy 719 CAGTTTCTACGAGTGTCTGATCAAAAGGACTTTGGACTAAAGTCTGATGAACCTTCCCAATCAG 778
Db 1 CAGTTTACGAGCTGTTGA-CAAAGGCACCTGGACTAAAGTCTGATGACCTTCCAATCCAG 59
Qy 779 ATGAGCATGATGATTTGGCCAGAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAG 838
Db 60 ATGAGCATGATGATTTGGCCAGAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAG 119
Qy 839 ACNAGGCCAGAGTGTCTCAAAATCTTTGACGGCACAGATCGCTGTGTGACTCCGGTTCTG 898
Db 120 ACNAGGCCAGAGTGTCTCAAAATCTTTGACGGCACAGATCGCTGTGTGACTCCGGTTCTG 179
Qy 899 ACTTTTGAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGT 958
Db 180 ACTTTTGAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGT 239
Qy 959 GAGGAGCAGGACGTTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCT 1018
Db 240 GAGGAGCAGGACGTTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCT 299
Qy 1019 TCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGA 1078
Db 300 TCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGA 359
Qy 1079 TTCAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTA 1138
Db 360 TTCAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTA 419
Qy 1139 AAAGCTAGTCTCTAACTTCCAGGCCACCGGCTC-AAAGTGAATTTGAATACCTGCAATTTACA 1197
Db 420 AAAGCTAGTCTCTAACTTCCAGGCCACCGGCTC-AAAGTGAATTTGAATACCTGCAATTTACA 479
Qy 1198 GTGTAGAGTAACACATAACATTTGATGATGCAATGGAACATGAGGAGAACAGTATTAAGTGT 1257
Db 480 GTGTAGAGTAACACATAACATTTGATGATGCAATGGAACATGAGGAGAACAGTATTAAGTGT 539
Qy 1258 CTACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCT 1317
Db 540 CTACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCT 599
Qy 1318 AAAAATGGTTATCATTTAGGGCTTTTGGATTTATAAACTTTGGGTACTTTATATAAAATTTAT 1377
Db 600 AAAAATGGTTATCATTTAGGGCTTTTGGATTTATAAACTTTGGGTACTTTATATAAAATTTAT 659
Qy 1378 GGTAGTATTCTGCCTCCAGTTTGCCTGATATATTTGTTGATATTAAGATTTCTTGACTT 1437
Db 660 GGTAGTATTCTGCCTCCAGTTTGCCTGATATATTTGTTGATATTAAGATTTCTTGACTT 719
Qy 1438 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATT-CTTGAAGACATC-GATATA 1495
Db 720 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATT-CTTGAAGACATCNGATATA 779
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QY 1496 CATTATTACACTCTT-GATTCTACAATGTAGAAA 1531
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Db 780 CATTATTACACTCTTGGATCTACAATGGTAGAAA 816
|||||

RESULT 13
US-11-266-748A-137395/c
; Sequence 137395, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 137395
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)..(52)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (152)..(152)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-137395

Query Match 45.3%; Score 734.6; DB 8; Length 924;
Best Local Similarity 97.7%; Pred. No. 8.3e-133;
Matches 798; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

QY 719 CAGTTCTACAGCTGCTGATCAAGGACTTGGACTAAAGTCTGTAGAACTTCCCAATCAG 778
Db 924 CAGTTTACAGCTGTTGA-CAAAGGCACTGGACTAAAGTCTGTAGACCTTCCAATCCAG 866
QY 779 ATGAGCATGATGATGGCCAGAAATCAAGAGAAAGTTTCAGATGATTTTCAAGAAAG 838
Db 865 ATGAGCATGATGATGGCCAGAAATCAAGAGAAAGTTTTCAGATGATTTTCAAGAAAG 806
QY 839 ACGAAGGAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTTCTG 898
|||||

Db 805 ACGAAGCCAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTTCTG 746
QY 899 ACTTTTGGAGGTTGTTTCATCATCATCATCATCAACAACAGGAAACGGGCTCGTTTATACCACT 958
|||||
Db 745 ACTTTTGGAGGTTGTTTCATCATCATCATCATCAACAACAGGAAACGGGCTCGTTTATACCACT 686
|||||
QY 959 GAGGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACACCCAGCCATCCCT 1018
|||||
Db 685 GAGGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACACCCAGCCATCCCT 626
|||||
QY 1019 TCTTTCAAAGGGATCCTTTTATAGAGAAACACACCTGAGGAGATACCTTGAAGAATTTGA 1078
|||||
Db 625 TCTTTCAAAGGGATCCTTTTATAGAGAAACACACCTGAGGAGATACCTTGAAGAATTTGA 566
|||||
QY 1079 TFCAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTA 1138
|||||
Db 565 TFCAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTA 506
|||||
QY 1139 AAAGCTAGTCTCTAACTTCCAGGGCCACGGCTC-AAAGTGAATTTGAATACTGCATTTACA 1197
|||||
Db 505 AAAGCTAGTCTCTAACTTCCAGGGCCACGGCTC-AAAGTGAATTTGAATACTGCATTTACA 446
|||||
QY 1198 GTGTAGAGTAACATACATTAATGTATGATGGAACATGGAGGAACAGTATTACAGTGTCT 1257
|||||
Db 445 GTGTAGAGTAACATACATTAATGTATGATGGAACATGGAGGAACAGTATTACAGTGTCT 386
|||||
QY 1258 CTACCACCTCTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGATGATTGAATTC 1317
|||||
Db 385 CTACCACCTCTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGATGATTGAATTC 326
|||||
QY 1318 AAAAATGTTTATCATTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTTATCTAAATTTAT 1377
|||||
Db 325 AAAAATGTTTATCATTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTTATCTAAATTTAT 266
|||||
QY 1378 GGTAGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTT 1437
|||||
Db 265 GGTAGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTT 206
|||||
QY 1438 ATATTTTGAATGGGTTCTAGTGAAAGAAAGAAATGATATATTTCTTGAAGACATC-GATATA 1495
|||||
Db 205 ATATTTTGAATGGGTTCTAGTGAAAGAAAGAAATGATATATTTCTTGAAGACATCNGATATA 146
|||||
QY 1496 CATTATTATACACTCTT-GATTCTACAATGTAGAAA 1531
|||||
Db 145 CATTATTATACACTCTTGGATTTCTACAATGGTAGAAA 109
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RESULT 14
US-11-344-932-74
; Sequence 74, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota

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/ APPLICANT: Foy, Teresa M.
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Meagher, Madeleine Joy
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C32
/ CURRENT APPLICATION NUMBER: US/11/344,932
/ PRIOR FILING DATE: 2006-02-01
/ PRIOR FILING DATE: 2002-05-09
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR FILING DATE: 2001-05-09
/ PRIOR FILING DATE: 2001-05-09
/ PRIOR FILING DATE: 2001-05-09
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR FILING DATE: 2001-01-12
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/ PRIOR FILING DATE: 2000-11-09
/ PRIOR FILING DATE: 2000-10-10
/ PRIOR FILING DATE: 2000-10-10
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR FILING DATE: 2000-09-06
/ Remaining Prior Application data removed - See File Wrapper or PALM.
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/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 74
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 317, 430
/ OTHER INFORMATION: n = A,T,C or G
US-11-344-932-74

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Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Qy 1156 TCCAGGCCACCGCTCAAGTGAATTTGAATCTAGTCTAGTACAGTACAGTAAACATATA 1215
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Qy 1216 CATTGTATGATGGAACATGAGGACAGATTTACAGTGCTCCTACCACTCTAATCAAGA 1275
Db 181 CATTGTATGATGGAACATGAGGACAGATTTACAGTGCTCCTACCACTCTAATCAAGA 240

Qy 1276 AAAGAATTTACAGACTCTGATTTCTACAGTGATGAATTTCTAAATAATGGTTATCATTAG 1335
Db 241 AAAGAATTTACAGACTCTGATTTCTACAGTGATGAATTTCTAAATAATGGTTATCATTAG 300

Qy 1336 GGCCTTTGATTTATAAACTTTGGGTACTTATCTAAATATAGTAGTATTCGCCCTTC 1395
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Qy 1396 CAGTTTGGCTTGATATATTGTTGATTAAGATTTCTGACTTATATTGTTGAATGGGTTCT 1455
Db 361 CAGTTTGGCTTGATATATTGTTGATTAAGATTTCTGACTTATATTGTTGAATGGGTTCT 420

/ APPLICANT: Foy, Teresa M.
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Meagher, Madeleine Joy
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C32
/ CURRENT APPLICATION NUMBER: US/11/344,932
/ PRIOR FILING DATE: 2006-02-01
/ PRIOR FILING DATE: 2002-05-09
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR FILING DATE: 2001-05-09
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/ PRIOR FILING DATE: 2000-10-10
/ PRIOR FILING DATE: 2000-10-10
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR FILING DATE: 2000-09-06
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 74
/ LENGTH: 537
/ TYPE: DNA
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/ FEATURE:
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/ OTHER INFORMATION: n = A,T,C or G
US-11-344-932-74

Query Match 31.8%; Score 515; DB 10; Length 537;
Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1036 TTTTCATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTTCAGCCGCGAAGAGAT 1095
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Qy 1096 TTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTCTAACT 1155
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
6976.201 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
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12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1532.6	94.5	1544	6	CR615811 full-leng
4	1455.6	89.8	1598	6	CR618063 full-leng
5	1367.8	84.4	1606	6	CR857309 Pongo pyg
6	935.2	57.7	1042	4	BX359836 BX359836
7	916.4	56.5	977	1	AL558928 AL558928
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9	887.6	54.8	924	4	BX449004 BX449004
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12	848.8	52.4	955	2	BG741165 602631843
13	845.8	52.2	1076	1	AL555978 AL555978
14	822.2	50.7	990	1	AL551698 AL551698
15	813.6	50.2	823	3	BM723657 UI-E-EJ0-
16	807.4	49.8	1523	6	AK002401 Mus muscu
17	807.4	49.8	2576	6	AK048249 Mus muscu
18	801	49.4	1558	6	AK160586 Mus muscu
19	794.4	49.0	893	1	AL558977 AL558977

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21	747	46.1	890	3	BQ962523
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25	726.4	44.8	890	3	BQ941482
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ALIGNMENTS

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ACCESSION CR625004.1 GI:50505811
VERSION CR625004.1
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1967)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization.
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1967)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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VERSION CR616479.1 GI:50497286
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 3111)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.
Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1381 AGTTAATCTGCCCTCCAGTTTGTGATATATTTGTTGATATAAAGATTCTTGACTTATA 1440
DB 1453 AGTTAATCTGCCCTCCAGTTTGTGATATATTTGTTGATATAAAGATTCTTGACTTATA 1512
QY 1441 TTTTGAATGGTCTTAGTGAAAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
DB 1513 TTTTGAATGGTCTTAGTGAAAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1572
QY 1501 ATTTACACTCTGATCTTACAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGTGTAT 1560
DB 1573 ATTTACACTCTGATCTTACAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGTGTAT 1632
QY 1561 AAAAGTCACGTGAAAAA 1579
DB 1633 AAAAGTCACGTGAAAAA 1651

```

RESULT 3

CR615811

LOCUS

DEFINITION

1544 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI027YJ12 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION

CR615811

VERSION

CR615811.1 GI:50496618

KEYWORDS

HTC; CNSLT_cDNA.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1544)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paradise Avenue

2 (bases 1 to 1544)

REFERENCE

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source Location/Qualifiers
1..1544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI027XJ12"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 94.5%; Score 1532.6; DB 6; Length 1544;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1535; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCATGGCATCGAGGCGATCTCGTTCATGGAGCTGTCGGCCTGGCCCCGGGCGCGGTT 60
Db 6 CGCATGGCATCGAGGCGATCTCGTTCATGGAGCTGTCGGCCTGGCCCCGGGCGCGGTT 65

Qy 61 CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 120
Db 66 CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 125

Qy 121 CCGCTACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 180
Db 126 CCGCTACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 185

Qy 181 GCCCGGGAGCGCGCTGCTCGCGCTGTGTGCAAGCGGTGCGATGCTGTGTGAGCC 240
Db 186 GCCCGGGAGCGCGCTGCTCGCGCTGTGTGCAAGCGGTGCGATGCTGTGTGAGCC 245

Qy 241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCGAGCGGGA 300
Db 246 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCGAGCGGGA 305

Qy 301 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
Db 306 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 365

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTTCTCTCAAAAATTTGGCAGAG 420
Db 366 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTTCTCTCAAAAATTTGGCAGAG 425

Qy 421 TGGTGAGAACTCGTATGCCCGCTGAATCTCTGCTGACCTTCTGCTGGTGGCTTAT 480
Db 426 TGGTGAGAACTCGTATGCCCGCTGAATCTCTGCTGACCTTCTGCTGGTGGCTTAT 485

Qy 481 GTGTGCACTGGGCATTATTAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGCTCAGGT 540
Db 486 GTGTGCACTGGGCATTATTAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGCTCAGGT 545

Qy 541 CATTGATGCAAAATATGGTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAAAACCTCA 600
Db 546 CATTGATGCAAAATATGGTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAAAACCTCA 605

Qy 601 GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGACATGTTGGATGGTGGAGCACCTTT 660
Db 606 GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGACATGTTGGATGGTGGAGCACCTTT 665

Qy 661 CTATACGACTTACAGCACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 666 CTATACGACTTACAGCACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 725

Qy 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATTCAGAT 780
Db 726 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATTCAGAT 785

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Db 786 GAGCATGATGATTTGGCCAGAAATGAGAGAAATTTGCAGATGATTTTCAGAGAGAC 845

Qy 841 GAAGGAGAGTGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGAGCTCCGGTTCTGAC 900

Db 846 GAAGGAGAGTGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGAGCTCCGGTTCTGAC 905

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Db 966 GGAGCAGAGCTGAGCGCCCGCTGCACCTCTGCTGTGTAAACACACCCAGCCATCCCTTC 1025

Qy 1021 TTTCAAAAGGATCTTTTCATAGAGAAACAACATGAGGAGATATCTTGAAGAAATTTGAT 1080

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Db 1086 CAGCGCGAGAGATTTATCAGCTTAACTCAGATAAATCATTCAGAAATTAAGGTAAA 1145

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Db 1146 AGCTAGTCTCTAACTCCAGGCCCAAGCTCAAGTGAATTTGAATCTACATTTACAGTG 1205

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Qy 1261 CCAGTCTAACTCAAGAAAGAAATTTACAGCTCTGATCTACAGTGAATTTGAATTTCTAAA 1320

Db 1266 CCAGTCTAACTCAAGAAAGAAATTTACAGCTCTGATCTACAGTGAATTTGAATTTCTAAA 1325

Qy 1321 AATGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTATAATTTAGGT 1380

Db 1326 AATGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTATAATTTAGGT 1385

Qy 1381 AGTTATTTCCCTCCAGTTTGTGTGATATATTTTGTGATTAATTAAGATTTCTTGACTTATA 1440

Db 1386 AGTTATTTCCCTCCAGTTTGTGTGATATATTTTGTGATTAATTAAGATTTCTTGACTTATA 1445

Qy 1441 TTTTGAATGGTCTAGTGAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1500

Db 1446 TTTTGAATGGTCTAGTGAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1505

Qy 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAA 1539

Db 1506 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAA 1544

RESULT 4
CR618063
LOCUS full-length cDNA clone CS0DM013Y103 of Fetal liver of Homo sapiens (human).
DEFINITION
CR618063
VERSION CR618063.1 GI:50498870
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1598)
AUTHORS Li W.B., Gruber C., Jesse J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1598)

AUTHORS TITLE JOURNAL

Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES source

Location/Qualifiers
1..1598
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM013V103"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 89.8%; Score 1455.6; DB 6; Length 1598;
Best Local Similarity 96.9%; Pred. No. 8.2e-313;
Matches 1513; Conservative 0; Mismatches 4; Indels 45; Gaps 1;
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2 CGCCATGGCACTGCAGGCGATCTCGGTTCATGGAGCTGTCCGGCTCGGCCCGGCCCGGT 141
3 CTGTGCTATGGTCTCGGTGACTTTCGGGGCGCTGTGTGACGCGTGGACCGGCCCGGCTC 120
4 CTGTGCTATGGTCTCGGTGACTTTCGGGGCGCTGTGTGACGCGTGGACCGGCCCGGCTC 201
5 CGCTACGAGCTGAGCGGCTTGGCCGGGCGGCTGTGTGACGCGTGGACCGGCCCGGCTC 180
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7 GCCCGGGGAGCGCGCTGTGCGGGCTGTGTGCAAGCGGTGCGATGTGTGCGGAGCC 240
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13 AGCTGCCACCATATCAACTATTTGCTTTGTGAGGCTTCTCTCAAAAATTGGCAGAA 420
14 AGCTGCCACCATATCAACTATTTGCTTTGTGAGGCTTCTCTCAAAAATTGGCAGAA 501
15 TGTGAGAACTCCATATGCCCCGTGAATCTCTGGGTGACTTTGCTGGTGGTGGCTTAT 480
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20 CATTGATGCAATAT 636
21 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 660
22 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 696
23 CTATAGCACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGAGCAATGAAACCCCA 720
24 CTATAGCACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGAGCAATGAAACCCCA 756
25 GTTCTACGAGCTCTGATCAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 780

757 GTTCTACGAGCTCTGATCAAGAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 816
781 GAGCATGATGATTTGCCAGAAATGAAGAGAGTTCAGATGATATTTTGCAGAGAAC 840
817 GAGCATGATGATTTGCCAGAAATGAAGAGAGTTCAGATGATATTTTGCAGAGAAC 876
841 GAAGGCAGAGTGTGTCAAACTTTTGCAGGACAGATGCTGTGTGACTTCCGGTCTGAC 900
877 GAAGGCAGAGTGTGTCAAACTTTTGCAGGACAGATGCTGTGTGACTTCCGGTCTGAC 936
901 TTTTGAAGAGTGTGTTCATCATGATCAAAAGGAAACGGGGCTCGTTTATCACAGTGA 960
937 TTTTGAAGAGTGTGTTCATCATGATCAAAAGGAAACGGGGCTCGTTTATCACAGTGA 996
961 GGAGCAGGAGCTGAGCCCGCCCTGCACTCTGCTGTGTAAACACCCAGCCATCCCTTC 1020
997 GGAGCAGGAGCTGAGCCCGCCCTGCACTCTGCTGTGTAAACACCCAGCCATCCCTTC 1056
1021 TTTTAAAGGAGTCTTTTATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
1057 TTTTAAAGGAGTCTTTTATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1116
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1177 AGCTAGTCTTAACTTCCAGGCCCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1236
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1417 AGTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1476
1441 TTTTGAATGGTCTTAGTGAAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
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1561 AA 1562
1597 AA 1598

RESULT 5

CR857309
LOCUS
DEFINITION
Pongo pygmaeus mRNA; cDNA DKFp46901232 (from clone DKFp46901232).
ACCESSION
CR857309
VERSION
CR857309.1
GI:55725646
KEYWORDS
HTC.
SOURCE
Pongo pygmaeus (orangutan)
ORGANISM
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo.
REFERENCE
1 (bases 1 to 1606)

AUTHORS Bahr, A., Lauber, J., Mewes, H. W., Weil, B., Amid, C., Oeanger, A.,
FOBO, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olgien (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp46901232) is available at the RZPD Deutsches
Reisourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?ClonedID=DKFZp46901232
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/
FEATURES
Location/Qualifiers
1..1606
/organism="Pongo pygmaeus"
/mol_type="mRNA"
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/tissue_type="kidney"
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DH10B; sites SfiIA + SfiIB"
/dev_stages="adult"
/note="alpha-methylacyl-CoA racemase (Homo sapiens)"
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/gene="DKFZp46901232"
96..1244
/gene="DKFZp46901232"
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/protein_id="CAH89605.1"
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Best Local Similarity 97.1%; Pred. No. 2.4e-293;
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DB 92 CGCCATGCGACTGACGGGCACTCGGTATGGAGCTGTCCGGCTTGGCCCGGGCCCGTT 151
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DB 152 CTGTGCTAAGGTTCCTAGCGGACTTCGGGGCGCGGTGTGTACCGTGGACCGCGCTCGGCTC 211
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DB 332 CTTCCGCGCGGTGTGTCATGGAGAACTCCAGCTGGGGCCAGAGATTCGTGACGCGGAAAA 391
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QY 1201 TAGAGTAAACATAAACAATTTGATGCAATGGAAACATGAGGAGACAGTATTACAGTGTCTTA 1260
DB 1292 TAGGTTAAACATAAACAATTTGATGCAATGGAAACATGAGGAGACAGTATTACAGTGTCTTA 1351
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DB 1352 CCAGCTTAACTCAAGAAAGAAATTTATGACACTGATTTCTACAGTGAATGATTTGAAATCTAAA 1411
QY 1321 AATGGTTATCAATAGGCTTTTGAATTTATAAAA-ACTTTGGGTACTTATACATAAATTTATGG 1379
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DB 1472 TAGTTATCTGCTTCCAGTTTGGCTG-----ATATATTGTTGATATTAAGATTTCTTGA 1531
QY 1435 CTTATATTTTGAATGGGTT 1453

Db 1532 CTTATATTTGAATGGTT 1550

RESULT 6
BX359836 1042 bp mRNA linear EST 23-APR-2004
LOCUS BX359836 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1062Y019 5-PRIME, mRNA sequence.
ACCESSION BX359836
VERSION BX359836.2 GI:46554896
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1042)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30384374.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2801.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0D1062AH10QP1&c=2801.r.

FEATURES
source Location/Qualifiers
1..1042
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0D1062Y019"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was
normalized. Library was constructed by Life technologies, a
division of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 57.7%; Score 935.2; DB 4; Length 1042;
Best Local Similarity 94.8%; Pred. No. 4.4e-197;
Matches 961; Conservative 32; Mismatches 15; Indels 6; Gaps 3;
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Db 14 CGCCATGACATGACAGGCGATCTCGGTCTATGAGCTGTCCGGCTGCGCCCGGCGCGTT 73
QY 61 CTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 74 CTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 133
QY 121 CGCTACGACATGACAGGCGCTGTGGCGCGGCGCAAGCGCTCGTAGTCTGACCTGAAGCA 180
Db 134 CGCTACGACATGACAGGCGCTGTGGCGCGGCGCAAGCGCTCGTAGTCTGACCTGAAGCA 193
QY 181 GCGCGGGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 194 GCGCGGGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
QY 241 CTTCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 254 MTMMGMSMGSGTGTATGAGAAATCCAGCTGGGCCCGAGAGATTCTGACGCGGAAAA 313
QY 301 TCCAAAGCTTATTATGACAGGCTGAGTGGATTGTCAGTGGAGGCTTCTGCGGTT 360

Db 314 TCCAAAGCTTATTATGACAGGCTGAGTGGATTGTCAGTCCAGTCCAGAAAGCTTCTGCGGTT 373
QY 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAG 420
Db 374 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAG 433
QY 421 TGGTCCAGAAATCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 434 TGGTCCAGAAATCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
QY 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 494 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
QY 541 CATTGATGCAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 554 CATTGATGCAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
QY 601 GAAATCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 614 GAAATCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
QY 661 CTATACGACTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 720
Db 674 CTATACGACTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 733
QY 721 GTTCTACGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 734 GTTCTACGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
QY 781 GAGCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 794 GAGCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
QY 841 GAAGCAGAGTGTGTCAAAATTTGACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 900
Db 854 GAAGCAGAGTGTGTCAAAATTTGACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 913
QY 901 TTTTCAGGAGTGTGTCAAAATTTGACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 960
Db 914 TTTTCAGGAGTGTGTCAAAATTTGACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 970
QY 961 GGAGCAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
Db 971 AGGAGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021

RESULT 7

AL558928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL558928 977 bp mRNA linear EST 02-APR-2004
AL558928 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ007Y107 5-PRIME, mRNA sequence.

AL558928
AL558928
AL558928.3 GI:46184315
EST.

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 977)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283061.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster 2801.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?c=CS0DJO07AE04QP1&c=2801.r>.

FEATURES

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/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="CS0DJO07Y107"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo (dtr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

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Query Match      56.5%; Score 916.4; DB 1; Length 977;
Best Local Similarity 99.4%; Pred. No. 6.6e-193;
Matches 928; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CGCCATGCACTGCAGGCGATCTCGTTCATGGAGCTGTCGGCCCTGGCCCGGCCCGGTT 60
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Qy 61 CTGTGCTATGCTCGGCTGACTTCGGGGCGGCTGTGTGAGCGTGGACCGCCCGGCTC 120
Db 101 CTGTGCTATGCTCGGCTGACTTCGGGGCGGCTGTGTGAGCGTGGACCGCCCGGCTC 160

Qy 121 CGCTACGACGTCAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180
Db 161 CGCTACGACGTCAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 220

Qy 181 GCCCGGGGAGCGCGCTGCTCGGCGCTGTGTGAGCGGTGGATGCTGTCTGGAGCC 240
Db 221 GCCCGGGGAGCGCGCTGCTCGGCGCTGTGTGAGCGGTGGATGCTGTCTGGAGCC 280

Qy 241 CTTCCGCGCGGTGTTCATGGAAACTCCAGCTGGGCGCCAGAGATTCGACAGCGGAA 300
Db 281 CTTCCGCGCGGTGTTCATGGAAACTCCAGCTGGGCGCCAGAGATTCGACAGCGGAA 340

Qy 301 TCCAAAGGCTTATTTATGCCAGGCTCAGTGGATTTGGCCAGTCAGAACTTCTGCCGTT 360
Db 341 TCCAAAGGCTTATTTATGCCAGGCTCAGTGGATTTGGCCAGTCAGAACTTCTGCCGTT 400

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGTGTCTCTCAAAAATGGCAGAG 420
Db 401 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGTGTCTCTCAAAAATGGCAGAG 460

Qy 421 TGGTGAGAAATCCGTATGCCCGCTCAATCTCTCGCTGACTTTGCTGGTGGGCTTAT 480
Db 461 TGGTGAGAAATCCGTATGCCCGCTCAATCTCTCGCTGACTTTGCTGGTGGGCTTAT 520

Qy 481 GTGTGCACTGGGCAATTAATAGGCTCTTTTGAACCGCACAGCACTGCAAGGTCAGGT 540
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Qy 541 CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTCTTTTCTGTGGAAACTCA 600
Db 581 CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTCTTTTCTGTGGAAACTCA 640

Qy 601 GAAATCGAGTCTGTGGAGGACCTTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 660
Db 641 GAAATCGAGTCTGTGGAGGACCTTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 700

Qy 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGCGTGTGTGAGCAATAGAACCCA 720
Db 701 CTATACGACTTACAGGACAGAGATGGGAAATTCATGCGTGTGTGAGCAATAGAACCCA 760

Qy 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGAATCTCCCAATCAGAT 780
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Db 761 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGAATCTCCCAATCAGAT 820
Qy 781 GAGCATGATGATTGGCCAGAAATGAAGAAAGATTGGCAGATGATTGGCAAGAAGAC 840
Db 821 GAGCATGATGATTGGCCAGAAATGAAGAAAGATTGGCAGATGATTGGCAAGAAGAC 880
Qy 841 GAAGGACAGTGTGTCAAAATCTTTGACGGCAGATGCGTGTGACTCGGTTCTGAC 900
Db 881 G-ARGSAGATGGTGTCAAAATCTTTGACGGCAGATGCGTGTGACTCGGTTCTGAC 939
Qy 901 TTTTGACGAGTGTTCATCATGATCACAACAAG 934
Db 940 TTTTGACGAGTGTTCATCATGATCACAACAAG 973

RESULT 8
LOCUS      AY609940      1534 bp      mRNA      linear      HTC 31-JAN-2005
DEFINITION Sus scrofa clone Clu_4587.scr.msk.pi.Contigl, mRNA sequence.
ACCESSION  AY609940
VERSION     AY609940.1 GI:52351510
KEYWORDS   HTC.
SOURCE      Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Mammalia.
REFERENCE   1 (bases 1 to 1534)
            Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M.
            and Schierup,M.H.
            Comparative analysis of protein coding sequences from human, mouse
            and the domesticated pig
            (er) BMC Biol. 3 (1), 2 (2005)
            15679890
REFERENCE   2 (bases 1 to 1534)
            Hornshoj,H., Bendixen,C. and Panitz,F.
            Direct Submission
            Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
            Institute of Agricultural Sciences, Research Centre Foulum, Postbox
            50, Tjele DK-8830, Denmark
FEATURES             Location/Qualifiers
     source           1..1534
                     /organism="Sus scrofa"
                     /mol_type="mrna"
                     /db_xref="taxon:9823"
                     /clone="Clu_4587.scr.msk.pi.Contigl"
     misc_feature     1..1534
                     /note="similar to NM_014324.4 Homo sapiens
                     alpha-methylacyl-CoA racemase (AMACR), transcript variant
                     1"

ORIGIN
Query Match      56.5%; Score 915.6; DB 6; Length 1534;
Best Local Similarity 80.0%; Pred. No. 1.1e-192;
Matches 1137; Conservative 0; Mismatches 259; Indels 26; Gaps 4;

Qy 1 CGCCATGCACTGCAGGCGATCTCGGTTCATGGAGCTGTCGGCCCTGGCCCGGCCCGGTT 60
Db 84 CGCCAGGCGCGCTGCAGGCGGTTCCGGGTCTGTGAGCTGCGCGCTGGCCCGGCCCGGTT 143

Qy 61 CTGTGCTATGGTCTGTGCTGACTTTCGGGCGCGGTGTGTTAGCGGTGGACCGCCCGGCTC 120
Db 144 CTGCGGTATGGTCTGTGCGGACTTTCGGGGCGCAGGTGGTGTGTAGACCGCCCGGCTC 203

Qy 121 CCGCTACGACGTGAGCGCTTGGCGCGGGGCAAGCGTCTCGCTAGTGTGGACCTGAAGCA 180
Db 204 CCCTGGGACCCGAGACCCCTTGGCCCGGGGCAAGCGTCTCGTGTGTGGAACCTGAAGCT 263

Qy 181 GCCCGGGGAGCCCGCGGTGTGTGCGCGCTGTGTGCAAGCGGTGCGATGTGTCTGTGGAGCC 240
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QY 887 ACTCGGTTCTGACATTTTGGAGAGGTTGTTTCATCATGATCAACAAGAAACGGGGCTCG 946
Db 675 ACTCGGTTCTGACATTTTGGAGAGGTTGTTTCATCATGATCAACAAGAAACGGGGCTCG 616
QY 947 TTTATCACAGTGAGGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTGTTAAACACC 1006
Db 615 TTTATCACAGTGAGGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTGTTAAACACC 556
QY 1007 CCAGCCATCCCTTCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTT 1066
Db 555 CCAGCCATCCCTTCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTT 496
QY 1067 GAAGAATTTGGATTGAGCGCGAAGAGATTATTCAGCTTAATCAGATAAAATCATTTGAA 1126
Db 495 GAAGAATTTGGATTGAGCGCGAAGAGATTATTCAGCTTAATCAGATAAAATCATTTGAA 436
QY 1127 AGTAATAAGGTAAGGTAAGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATA 1186
Db 435 AGTAATAAGGTAAGGTAAGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATA 376
QY 1187 CTGCATTTACAGTGTAGAGTAACACATAACATTTGTATGTCATGGAACACATGAGGAAACAGT 1246
Db 375 CTGCATTTACAGTGTAGAGTAACACATAACATTTGTATGTCATGGAACACATGAGGAAACAGT 316
QY 1247 ATTACAGTGTCTACACTCTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTAT 1306
Db 315 ATTACAGTGTCTACACTCTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTAT 256
QY 1307 GATTCGAATTTCTAAAATGTTTATCATTTAGGGCTTTTGTATTTATAAACTTTGGGTACTTA 1366
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QY 1367 TACTAAATTTAGTGTAGTATTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAG 1426
Db 195 TACTAAATTTAGTGTAGTATTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAG 136
QY 1427 ATCTTGACTTATATTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTGAAGAC 1486
Db 135 ATCTTTSACTATATTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTGAAGAC 76
QY 1487 ATCGATATACATTTATTTACACTCTTGTATTTACAAATGTAGAAAATGAGGAAATGCCACA 1546
Db 75 ATCGATATACATTTATTTACACTCTTGTATTTACAAATGTAGAAAATGAGGAAATGCCACA 16
QY 1547 AATTGTATG 1555
Db 15 AATTNNATB 7
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RESULT 10
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LOCUS
DEFINITION
AL571115 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CS0D1027YJ12 3-PRIME, mRNA sequence.
ACCESSION
AL571115
VERSION
AL571115.3 GI:46237222
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 971)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31292520.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2801.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?s=CS0D1027DE06NP1&c=2801.r>.

FEATURES

source

Location/Qualifiers

1..971

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1027YJ12"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

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Query Match 54.4%; Score 882.2; DB 1; Length 971;
Best Local Similarity 96.3%; Pred. No. 2.7e-185;
Matches 893; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

QY 612 TGTGGGAAGCACCTCTGAGGACAGACATGTTGGATGCTGGGACACCTTCTATACGACTT 671
Db 926 YGTGTGAACCCCTCGRMGACAGACATGTGANTGGT-GRGCACCTTTTCWMAACAAC 868
QY 672 ACAGCAGCAGCAGATGGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTCCTACGAGC 731
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QY 732 TGCTGATCAAGGACTTTGGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGGATG 791
Db 807 TGCTGATCAAGGACTTTGGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGGATG 748
QY 792 ATTGGCCAGAAATCAAGAAAGTTTCAGATGTTTTCAGAAAGCAAGCAAGCAGAGT 851
Db 747 ATTGGCCAGAAATCAAGAAAGTTTCAGATGTTTTCAGAAAGCAAGCAAGCAGAGT 688
QY 852 GGTGTCAAACTTTTGACGGCAGACAGATGCTGTGTGACTCCGGTTCCTGACTTTTGAGGAGG 911
Db 687 GGTGTCAAACTTTTGACGGCAGACAGATGCTGTGTGACTCCGGTTCCTGACTTTTGAGGAGG 628
QY 912 TTGTTTCATGATGATCAACAAGGAAACGGGGCTCGTTTATCATCCAGTGTAGGAGCAGAGC 971
Db 627 TTGTTTCATGATGATCAACAAGGAAACGGGGCTCGTTTATCATCCAGTGTAGGAGCAGAGC 568
QY 972 TGAGCCCCCGCCCTGACCTCTGCTGTTAAACCCCGACCCATCCCTTCTTTCAAAAGGG 1031
Db 567 TGAGCCCCCGCCCTGACCTCTGCTGTTAAACCCCGACCCATCCCTTCTTTCAAAAGGG 508
QY 1032 ATCTCTTTCATAGGAGAAACACACTGAGGAGATCTTTGAAGAATTTGGATTCAGCCGCGAAG 1091
Db 507 ATCTCTTTCATAGGAGAAACACACTGAGGAGATCTTTGAAGAATTTGGATTCAGCCGCGAAG 448
QY 1092 AGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAAGCTAGTCTCT 1151
Db 447 AGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAAGCTAGTCTCT 388
QY 1152 AACTTCCAGGCCACGGCTCAAGTGAATTTGAATATCTGCAATTTACAGTGTAGAGTAACAC 1211
Db 387 AACTTCCAGGCCACGGCTCAAGTGAATTTGAATATCTGCAATTTACAGTGTAGAGTAACAC 328
QY 1212 ATAACATTTGATGATGGAACACATGGAGAACACATATTACAGTGTCTCTACCACTCTAATC 1271
Db 327 ATAACATTTGATGATGGAACACATGGAGAACACATATTACAGTGTCTCTACCACTCTAATC 268
QY 1272 AAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGTAGTGAATTTCTAAAAATGGTTATCA 1331
Db 267 AAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGTAGTGAATTTCTAAAAATGGTTATCA 208
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QY 1332 TTAGGCTTTGATTTATAAACTTTGGGTACTTATATACTAAATATATGGTAGTTATTTCTGC 1391
 Db 207 TTAGGCTTTGATTTATAAACTTTGGGTACTTATATACTAAATATATGGTAGTTATTTCTGC 148
 QY 1392 CTTCCAGTTTGTGATATATTTGATATTAAGATTCTTGCATTTATATTTTGAATGG 1451
 Db 147 CTTCCAGTTTGTGATATATTTGATATTAAGATTCTTGCATTTATATTTTGAATGG 88
 QY 1452 TTCTAGTGAAGAAGGATGATATATTTCTTGAAGACATCGATATACATATTTATTTACACTCT 1511
 Db 87 TTCTAGTGAAGAAGGATGATATATTTCTTGAAGACATCGATATACATATTTATTTNACACTCT 28
 QY 1512 TGATTTCAATGTAGAAAATGAGGAA 1538
 Db 27 NGANNCTCAATGTAGAAAATGAGGAA 1

RESULT 11
 AL545355
 LOCUS
 DEFINITION 1081 bp mRNA linear EST 25-MAR-2004
 clone CS0D1027YJ12 5-PRIME, mRNA sequence.
 ACCESSION AL545355
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31267191.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 2801_r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0D1027DE06QP1&c=2801.r.

FEATURES
 source
 Location/Qualifiers
 1..1081
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1027YJ12"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
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 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 53.2%; Score 863; DB 1; Length 1081;
 Best Local Similarity 92.3%; Pred. No. 5.1e-181;
 Matches 939; Conservative 28; Mismatches 44; Indels 6; Gaps 6;
 QY 1 CGCCATGGCAGTCGAGGCGATCTCGGTCTATGGAGTGTCCGGCTCGGCCCGGCCGCTT 60
 Db 6 CGCCATGGCAGTCGAGGCGATCTCGGTCTATGGAGTGTCCGGCTCGGCCCGGCCGCTT 65
 QY 61 CTGTGCTATGTCCTGGTCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCCGGCTTC 120
 Db 66 CTGTGCTATGTCCTGGTCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCCGGCTTC 125

QY 121 CGCTACGACGTGAGCCGCTTTGGGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180
 Db 126 CGCTACGACGTGAGCCGCTTTGGGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 185
 QY 181 GCCGGGGAGGCGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTCCGATGTGCTGCTGAGCC 240
 Db 186 GCCGGGGAGGCGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTCCGATGTGCTGCTGAGCC 245
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 Db 246 CTTCCGCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCGCCAGAGATTTCTGCAGCGGAAAA 305
 QY 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCGCGTT 360
 Db 306 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCGCGTT 365
 QY 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAG 420
 Db 366 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAG 425
 QY 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTCTGGCTGACTTTGTGTTGGTGGCTTAT 480
 Db 426 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTCTGGCTGACTTTGTGTTGGTGGCTTAT 485
 QY 481 GTGTGCACTGGGCAATTAATATGGCTCTTTTGAACGCGCACAGCACTGCAAGGGTCAGGT 540
 Db 486 GTGTGCACTGGGCAATTAATATGGCTCTTTTGAACGCGCACAGCACTGCAAGGGTCAGGT 545
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 Db 546 CATTGATCAAAATATGGTGGAGAGAACAGCATATTTAAAGTTCTTTCTGTGGAAGAACTCA 605
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 Db 606 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGTGGAGAC-CTTT 664
 QY 661 CTATACGACTTACAGCACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCCA 720
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 QY 721 GTTCTACAGCTGTGATCAAAAGGACTTGGAGCTTAAAGTCTGATGAATTTCCCAATCAGAT 780
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 QY 841 GAAGGCAG-AGTGGTGTCAAAATCTTTGACGGCAC-AGATGGCTGTGTGACTCCCGTTCTG 898
 Db 844 GAAGGCAGTGTGGTGTAAATCTTTGACGGCACAAATGCTGTGTARCTCCGGTTCTT 903
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 Db 904 RCTTTTTRRRGGGKTGTATTAATATATAAAAAAGGAACGGGGTCG-TTATWACMAGT 962
 QY 959 GAGGAGCAGGAGCTGAGCCCGCTGCACTCTGCTGTTAAACACCCGAGCCATC 1015
 Db 963 AAGRGCC-GGACKTAGACCCCGCCACCCTTGTGTTAAAMCCCCCSCCTCCCTT 1018

RESULT 12
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 DEFINITION 602631843F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',
 mRNA sequence.
 ACCESSION BG741165
 VERSION BG741165.1 GI:14051818
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: James Cleaver, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10630 row: f column: 12
              High quality sequence stop: 805.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4776971"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP SKn3"
/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match      52.4%; Score 848.8; DB 2; Length 955;
Best Local Similarity 95.7%; Pred. No. 7.3e-178;
Matches 894; Conservative 0; Mismatches 37; Indels 3; Gaps 2;

Qy 154 GCGCTCGCTAGTGTGGACCTGAACGACGCGCGGAGCCGCTGTCGCGGCTGTG 213
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Db 61 CAAGCGGTGGAGTGTGCTGTGGAGCCCTTCGCGCGGCTGTGTCATGGAGAAATCCAGCT 120

Qy 274 GGGCCACAGATCTTGACGCGGGAATCCAAAGGCTTATTTATGCCAGGCTGAGTGAT 333
Db 121 GGGCCACAGATCTTGACGCGGGAATCCAAAGGCTTATTTATGCCAGGCTGAGTGAT 180

Qy 334 TGGCCAGTCAGGAAGCTTCTGCGGCTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 393
Db 181 TGGCCAGTCAGGAAGCTTCTGCGGCTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 240

Qy 394 AGGTGTTCTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGATATGCCCGCTGAATCTCCT 453
Db 241 AGGTGTTCTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGATATGCCCGCTGAATCTCCT 300

Qy 454 GCCTGACTTGTGTGTGGCTTATGTGTGCACTGGGCATTAATAATGGCTCTTTTGA 513
Db 301 GCCTGACTTGTGTGTGGCTTATGTGTGCACTGGGCATTAATAATGGCTCTTTTGA 360

Qy 514 CGGCACGCACTGACAGAGGTCAGGTCAATGATCAAAATGTTGGAGGAACAGCAT 573
Db 361 CGGCACGCACTGACAGAGGTCAGGTCAATGATCAAAATGTTGGAGGAACAGCAT 420

Qy 574 TTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 633
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Qy 634 GAACATGTTGATGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGAAT 693
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Qy 694 CATGCTGTGGAGCAATAGAACCCAGTTCTPACGAGCTGCTGATCAAAAGGACTTGGACT 753
Db 541 CATGCTGTGGAGCAATAGAACCCAGTTCTPACGAGCTGCTGATCAAAAGGACTTGGACT 600

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Qy 814 GTTTGCAGATGTTATTTGCAAAAGAGACGAGGACAGTGGTGCATAATCTTTGACGGCAC 873
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Qy 874 AGATGCTGTGTGACTCCGGTCTGACTTTTGGAGGAGTTGTTTCATCATGATCAACA 933
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Qy 934 GGAACGGGGTCTGTTTATCACCAGTGGAGGACGAGAC-GTGAGCCCCCGCTGCACCTC 992
Db 781 GGAACGGG--CTCGTTATCACCAGTGGAGGACGAGCGGTGAGCCCCCGCTGAACTCT 838

Qy 993 TGCTGTTTAAACACCCAGCCATCCCTCTTTTCAAAAGGATCCTTTTCATAGGAGAACACA 1052
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Qy 1053 CTGAGGAGATACCTTGAAGAATTTGGATTCAGCCG 1086
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RESULT 13
LOCUS      AL555978             1076 bp          mRNA          linear          EST 30-MAR-2004
DEFINITION AL555978 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
              cDNA clone CS0DK010Y111 5-PRIME, mRNA sequence.
ACCESSION  AL555978
VERSION     AL555978.3 GI:45860699
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE   1 (bases 1 to 1076)
AUTHORS     Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31277782.
             Contact: Genoscope
             Genoscope - Centre National de Sequencage
             2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
             was normalized. Library was constructed by Life Technologies, a
             division of Invitrogen. This sequence belongs to sequence cluster
             2801.r
             For more information about this cluster, see
             http://www.genoscope.cns.fr/cdna?s=CS0DK010AE06QPl&c=2801.r.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DK010Y111"
/cell_line="HELA"
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was
normalized."

ORIGIN
Query Match      52.2%; Score 845.8; DB 1; Length 1076;
Best Local Similarity 96.3%; Pred. No. 3.5e-177;

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Matches		891;	Conservative	14;	Mismatches	16;	Indels	4;	Gaps	4;
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Db	73	CGCATGCGACTG	CAGGCGATCTCG	GCATGAGCTG	TCGCGCTG	CGCCCGGCGCGCTT	132			
Qy	61	CTGTGCTATGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	120			
Db	133	CTGTGCTATGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	132			
Qy	121	CCGCTACGAGCT	GAGCGCGCTTGG	CGCGGCGCGCT	TCGCTAGCTG	TCGCTAGCTG	180			
Db	193	CCGCTACGAGCT	GAGCGCGCTTGG	CGCGGCGCGCT	TCGCTAGCTG	TCGCTAGCTG	252			
Qy	181	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	240			
Db	253	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	312			
Qy	241	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	300			
Db	313	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	372			
Qy	301	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	360			
Db	373	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	432			
Qy	361	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	420			
Db	433	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	492			
Qy	421	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	480			
Db	493	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	552			
Qy	481	GTGTGCACTGG	GCAT-TATAATGG	CTCTTTTAC	CGCACACG	CACGAGGT	539			
Db	553	GTGTGCACTGG	GCAT-TATAATGG	CTCTTTTAC	CGCACACG	CACGAGGT	612			
Qy	540	TCATTGATCAAT	ATATGCTGGAAG	GAACAGCATAT	TTAAGTTCT	TTTCTGGAACATC	599			
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Qy	600	AGAAATCGAGT	CTGTGGAGACCT	CGAGGACAGAA	CATGTTGGAT	GTGGAGCACCTT	659			
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Qy	660	TTATACGACTTA	CAGACAGAGAT	GCGGAATTCAT	GTGTTGAG	CAATAGAACCC	719			
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Qy	840	CGAAGCAGAGT	GGTGTCAAAAT	CTTTGACGG	CACAGCTG	CTGTGACTCCGGTCTGA	899			
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RESULT 14
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LOCUS
AL551698 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION
clone CS0D1062YP05 5-PRIME, mRNA sequence.
ACCESSION
AL551698

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

ORIGIN

Query Match
Best Local Similarity
Matches 855; Conservative 11; Mismatches 31; Indels 2; Gaps 2;

Qy	1	CGCCATGCGACTG	CAGGCGCATCTCG	GTCAATGAGCTG	TCGCGCTG	CGCCCGGCGCGCTT	60
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Qy	61	CTGTGCTATGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	120
Db	73	CTGTGCTATGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	132
Qy	121	CGCTACGAGCTG	AGCGCGCTTGG	CGCGGCGCGCT	TCGCTAGCTG	TCGCTAGCTG	180
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Qy	181	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	240
Db	193	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	252
Qy	241	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	300
Db	253	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	312
Qy	301	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	360
Db	313	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	372
Qy	361	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	420
Db	373	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	432
Qy	421	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	480
Db	433	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	492

AL551698.3 GI:45856497

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 990)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31273514.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

2801.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0D1062CH03QPl&c=2801.r.

Location/Qualifiers

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primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

50.7%; Score 822.2; DB 1; Length 990;

95.1%; Pred. No. 6.1e-172;

Matches 855; Conservative 11; Mismatches 31; Indels 2; Gaps 2;

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Db	73	CTGTGCTATGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	CTGCTGCTGCT	132
Qy	121	CGCTACGAGCTG	AGCGCGCTTGG	CGCGGCGCGCT	TCGCTAGCTG	TCGCTAGCTG	180
Db	133	CGCTACGAGCTG	AGCGCGCTTGG	CGCGGCGCGCT	TCGCTAGCTG	TCGCTAGCTG	192
Qy	181	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	240
Db	193	GCCGCGGAGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	CGCGCTGCTGCG	252
Qy	241	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	300
Db	253	CTTCCGCGCGGT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	GAGCGGAAAA	312
Qy	301	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	360
Db	313	TCCAAGGCTTAT	TATGCGAGGCT	GTATGAGAGAACT	CCAGCTGGG	CCAGAGATTCT	372
Qy	361	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	420
Db	373	AGCTGCGCAGAT	ATCAACTATTTGG	CTTGTGAGGCT	TCGCTGAGCT	TCGCTGAGCT	432
Qy	421	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	480
Db	433	TGCTGAGAAAT	CCGATGCGCGCT	GATCTCTCTG	GGTGGCTTAT	GGCTTAT	492


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ACCESSION
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VERSION
  BM723657.1 GI:19044988
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SOURCE
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    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homidae; Homo
REFERENCE
  1 (bases 1 to 823)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
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UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAGA; lens, CGATTAGGCA; eye anterior segment,
AATGCCGAT; optic nerve, CCAATAGTG; retina, CGCGC; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
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ORIGIN

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Query Match 50.2%; Score 813.6; DB 3; Length 823;
Best Local Similarity 99.1%; Pred. No. 4.9e-170;
Matches 816; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 361 GAGGACGAGGACGTGAGCCCGCCCTGCTGCTGTTAAACACCCAGCCATCCCT 420
Qy 1019 TCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGA 1078
Db 421 TCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGA 480
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Db 541 AAAGCTAGTCTCTAACTTCCAGGCCCGCCCTCAAGTGAATTTTGAATCTCATTTACAG 600
Qy 1199 TGTAGAGTAACACATAACATTTGATGATGAGAAACATGGAGGAAACAGTATTACAGTGTCC 1258
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:13:09 ; Search time 10436.3 Seconds
(without alignments)
9932.518 Million cell updates/sec

Title: US-09-232-880-107

Perfect score: 1621

Sequence: 1 cgccatgctactgcaggca.....aaaaaaaaaaaaaaaaaaaa 1621

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext*1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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2: gb_pat:*
3: gb_ph:*
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5: gb_pr:*
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9: gb_un:*
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13: gb_in:*
14: gb_on:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	1621	100.0	1621	2	AR588592 Sequence
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ALIGNMENTS

RESULT 1	BD070256	1621 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	Compounds for immunodiagnosis of prostate cancer and methods for their use.				
DEFINITION	BD070256				
ACCESSION	BD070256.1 GI:22615859				
VERSION	JP 2001513886-A/107.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (Bases 1 to 1621)				
AUTHORS	Xu,J. and Dillon,D.C.				
TITLE	Compounds for immunodiagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2001513886-A 107 04-SEP-2001;				
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	CC Topology: Linear;				
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	FT source				
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PC C12N5/10,	
PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,	
PC A61K37/02,	
CC C12N5/00	
CC Compounds for immunotherapy and diagnosis of prostate cancer	
CC and methods	
CC for their use	
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DEFINITION	Sequence	107 from patent US 6465611.				
ACCESSION	AR237203					
VERSION	AR237203.1	GI:27281861				
KEYWORDS	.					
SOURCE						
ORGANISM	Unknown.					
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JOURNAL
Patent: US 6512094-A 107 28-JAN-2003;
Corixa Corporation; Seattle, WA
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ORIGIN

Query Match 100.0%; Score 1621; DB 2; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 CTGTGCTATGGTCTCGGCTGACTTCGGGGCGGTGGTACCGGTGGAACGGGCCGGCTC 120

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DB 121 CGCTACGAGCTGAGCGGCTTGGCCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180

QY 181 GCGCGGGGAGCGCGTCTGCGGGCTGTGTGCAAGCGGTGGATGTCTGCTGGAGCC 240
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AR366923 1621 bp DNA linear PAT 12-SBP-2003
Sequence 107 from patent US 6329505.
AR366923
AR366923.1 GI:34599898
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1621)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
Compositions and methods for therapy and diagnosis of prostate
cancer
Patent: US 6329505-A 107 11-DEC-2001;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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DEFINITION Sequence 107 from patent US 6630305.
ACCESSION AR405226
VERSION AR405226.1 GI:40154063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 107 OCT-2003; Corixa Corporation; Seattle, WA; WOX;
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Qy 1621 A 1621
Db 1621 A 1621

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LOCUS AR439430 1621 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 107 from patent US 6664377.
ACCESSION AR439430
VERSION AR439430.1 GI:42665339
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1621)
AUTHORS Xu,J.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6664377-A 107 16-DEC-2003; Corixa Corporation, Seattle, WA;
FEATURES
source Location/Qualifiers
1..1621
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Query Match 100.0%; Score 1621; DB 2; Length 1621;
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Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	601	GAATATCAGATCTGTGGAGACACCTTCAGAGACAGAAATCTGTTGGATGGTGGACACCTTT	660
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Qy	1141	AGCTAGTCTTAACTTTCAGGCCACGGCTCAAGTGAAATTTGAATATCTGCAATTTACAGTG	1200
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Db	1441	TTTTGAATGGGTCTCTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCATATACATTT	1500
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DEFINITION	AR588592		
ACCESSION	AR588592		
VERSION	AR588592.1	GI:56635489	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1621)		
AUTHORS	Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6800746-A 107 05-OCT-2004;		
FEATURES	Corixa Corporation; Seattle, WA		
source	Location/Qualifiers		
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Query Match	100.0%;	Score 1621;	DB 2; Length 1621;
Best Local Similarity	100.0%;	Pred. No. 0;	
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Qy	121	CCGCTACGACTGAGCCGCTTGGGCCCGGGCAACGCGTCTGCTAGTGTGACCTCGAAGCA	180
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Qy	181	GCCCGGGAGCCCGCTGCTGCGCGCTGTGTGTGAACGGTTCGATGTGCTGTGAGCC	240
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LOCUS Sequence 107 from patent US 6818751.
DEFINITION AR605412
ACCESSION AR605412
VERSION AR605412.1 GI:56657076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6818751-A 107 16-NOV-2004;
Corixa Corporation; Seattle, WA
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LOCUS AR656751 1621 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 107 from patent US 6894146.
ACCESSION AR656751
VERSION AR656751.1 GI:67589829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6894146-A 107 17-MAY-2005;
Corixa Corporation; Seattle, WA
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DB 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGTTGGAGCACCTTT 660

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QY 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
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QY 1621 A 1621
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QY 1621 A 1621
Db |
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QY 1621 A 1621
Db 1621 A 1621

RESULT 2

US-09-030-607-107
; Sequence 107, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1621 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-09-030-607-107

Query Match

Best Local Similarity 100.0%; Score 1621; DB 3; Length 1621;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCCATGGCACTGCAGGCGATCTCGTCAATGAGCTGTCCGGCTCGCCGCGCCGCGCTT 60
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DB 61 CTGTGCTATGCTCTGGCTGACTTCGGGGCGGTGTGTACGCTGGACCGGCCGGCTC 120
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RESULT 3

US-09-439-313-107

; Sequence 107, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

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DB 841 GAAGGCAGAGTGGTCTCAAACTTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGAC 900
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QY 1621 A 1621
DB 1621 A 1621
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RESULT 3

US-09-439-313-107

; Sequence 107, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1621 A 1621
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RESULT 5

US-09-232-149A-107
; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGCACTGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTGGCCCGGCGCCGTT 60
Db 1 CGCCATGCACTGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTGGCCCGGCGCCGTT 60
Qy 61 CTGTGCTATGTCCTGCTGACTTTCGGGGCGGTGTGGTACGCGTGAACCGGCGCGCTC 120
Db 61 CTGTGCTATGTCCTGCTGACTTTCGGGGCGGTGTGGTACGCGTGAACCGGCGCGCTC 120
Qy 121 CCCTACGACGTGAGCCGCTTTGGCCCGGGCAAGCGCTCGTGTGCTGGAACCTGAAGCA 180
Db 121 CCCTACGACGTGAGCCGCTTTGGCCCGGGCAAGCGCTCGTGTGGAACCTGAAGCA 180
Qy 181 GCCCGGGGAGCCGCTGCTCGCGCGTGTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
Db 181 GCCCGGGGAGCCGCTGCTCGCGCGTGTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
Qy 241 CTTCCGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGAAAA 300
Db 241 CTTCCGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGAAAA 300
Qy 301 TCCAAGGCTTATTTATGCAAGCTGAGTGGATTTGGCCAGTCAGGAAAGCTTCTGCCGTT 360
Db 301 TCCAAGGCTTATTTATGCAAGCTGAGTGGATTTGGCCAGTCAGGAAAGCTTCTGCCGTT 360
Qy 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGCGAGAAG 420
Db 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATGCGAGAAG 420
Qy 421 TGGTGAGAACTCGGTATGCCCGCTGAATCTCCTCGCTGACTTTCGTGGTGGCTTAT 480
Db 421 TGGTGAGAACTCGGTATGCCCGCTGAATCTCCTCGCTGACTTTCGTGGTGGCTTAT 480
Qy 481 GTGTGCACTGGGCAATTAATGCTTTTGGCCGACACGCACTGCAAGGGTCAGGT 540
Db 481 GTGTGCACTGGGCAATTAATGCTTTTGGCCGACACGCACTGCAAGGGTCAGGT 540
Qy 541 CATTGATGCAATATGTTGGAGGAACAGCATATTTAAGTCTTCTGTGGAAAACTCA 600
Db 541 CATTGATGCAATATGTTGGAGGAACAGCATATTTAAGTCTTCTGTGGAAAACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780
Qy 781 GAGCATGATGATGGCCAGAAATCAAGAAAGTTTTCAGATGATTTTGAAGAAGAC 840
Db 781 GAGCATGATGATGGCCAGAAATCAAGAAAGTTTTCAGATGATTTTGAAGAAGAC 840
Qy 841 GAAGCAGAGTGGTCTCAAACTTTTGAAGCAGACAGATCCCTGTGTGACTCCGGTTCTGAC 900
Db 841 GAAGCAGAGTGGTCTCAAACTTTTGAAGCAGACAGATCCCTGTGTGACTCCGGTTCTGAC 900
Qy 901 TTTTGGAGAGGTGTTTATCATGATCAACAAAGAACCGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGGAGAGGTGTTTATCATGATCAACAAAGAACCGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGACGTGAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGACGTGAGCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTTCAAAAGGATTCCTTTATAGGAGAACACATGAGGAGATCTTTGAAGAAATTTGGATT 1080
Db 1021 TTTTCAAAAGGATTCCTTTATAGGAGAACACATGAGGAGATCTTTGAAGAAATTTGGATT 1080

Qy 1081 CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAA 1140
Db 1081 CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAA 1140
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Qy 1201 TAGAGTAACACATAAATGATGATGCAATGGAACATGGAGAACAGTATTAACAGTGCTTA 1260
Db 1201 TAGAGTAACACATAAATGATGATGCAATGGAACATGGAGAACAGTATTAACAGTGCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
Db 1261 CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAAAACTTTGGGTACTTATACAAATTTATGTT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAAAACTTTGGGTACTTATACAAATTTATGTT 1380
Qy 1381 AGTTATTCGCTTCCAGTTTGGTGGTATATTTGTTGATTTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTCGCTTCCAGTTTGGTGGTATATTTGTTGATTTAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGTCTAGTGAAGAAATGATATTTCTTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTAGTGAAGAAATGATATTTCTTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTGATTTCAAAATGAGAAATGAGGAAATGCCCAAAATTTGATGTTGAT 1560
Db 1501 ATTTACACTCTGATTTCAAAATGAGAAATGAGGAAATGCCCAAAATTTGATGTTGAT 1560
Qy 1561 AAAAGTCAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Db 1561 AAAAGTCAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 6
US-09-159-812-107
; Sequence 107, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428CS
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCCATGGCACTGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTGGCCCGGCGCCGTT 60
Db 1 CGCCATGGCACTGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTGGCCCGGCGCCGTT 60
Qy 61 CTGTGCTATGCTCTGCTGACTTTCGGGGCGGTGTGGTACGCGTGAACCGGCGCGGCTC 120
Db 61 CTGTGCTATGCTCTGCTGACTTTCGGGGCGGTGTGGTACGCGTGAACCGGCGCGGCTC 120

Db 1 CGCATGGCACTCAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTTGGCCCCGGGCCCGGTT 60
Qy 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCCGCTGTGTGTACGCTGGACCGGCCCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCCGCTGTGTGTACGCTGGACCGGCCCGGCTC 120
Qy 121 CCGTACGACGTGAGCGCTTGGGGCCGGGGCAAGGGCTCGTGTAGTCTGGACCTGAAGCA 180
Db 121 CCGTACGACGTGAGCGCTTGGGGCCGGGGCAAGGGCTCGTGTAGTCTGGACCTGAAGCA 180
Qy 181 GCCGGGGAGCCGCGCTGCTGGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240
Db 181 GCCGGGGAGCCGCGCTGCTGGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240
Qy 241 CTTCGGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCAGAGATTCGACAGCGGAAAA 300
Db 241 CTTCGGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCAGAGATTCGACAGCGGAAAA 300
Qy 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360
Db 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGCGAGAAG 420
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGCGAGAAG 420
Qy 421 TGGTGAAGATCCGTATGCCCGCTGAAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTAT 480
Db 421 TGGTGAAGATCCGTATGCCCGCTGAAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTAT 480
Qy 481 GTGTGCACTGGGCATTATAAGTGGCTTTTTTGACCGCACAGCACTGACAGGGTCAGGT 540
Db 481 GTGTGCACTGGGCATTATAAGTGGCTTTTTTGACCGCACAGCACTGACAGGGTCAGGT 540
Qy 541 CATTGATCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCA 600
Db 541 CATTGATCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGCATGAGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCATGAGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGTCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Db 721 GTTCTACGAGTCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Qy 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTCGAGATGATTTTGCAAAAGAAC 840
Db 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTCGAGATGATTTTGCAAAAGAAC 840
Qy 841 GAAGGACAGTGGTCAAACTTTTGACGGCACAGATCCCTGTGTGACTCCGGTCTGAC 900
Db 841 GAAGGACAGTGGTCAAACTTTTGACGGCACAGATCCCTGTGTGACTCCGGTCTGAC 900
Qy 901 TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGTGTTAAACACCCCGAGCCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGTGTTAAACACCCCGAGCCATCCCTTC 1020
Qy 1021 TTTCAAAAGGATTCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT 1080
Db 1021 TTTCAAAAGGATTCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT 1080
Qy 1081 CAGCGCGGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1140
Db 1081 CAGCGCGGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1140

Qy 1141 AGCTAGTCTTAATTCAGGCCCAAGTGAATTTGAATCTACTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTTAATTCAGGCCCAAGTGAATTTGAATCTACTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAAACATACATTAATGTCATGGAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Db 1201 TAGAGTAAACATACATTAATGTCATGGAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAGAAATTCAGACTCTGATTCACAGTGATGAATTTCTAAA 1320
Db 1261 CCACTCTAATCAAGAAAGAAATTCAGACTCTGATTCACAGTGATGAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATACTAAATTTATGGT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATACTAAATTTATGGT 1380
Qy 1381 AGTTATTTCTCCCTTCCAGTTTGTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTTCTCCCTTCCAGTTTGTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGGAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGGTTCTAGTGAAAGGAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTTGAATCTCAATGTAGAAAATGAGGAATGCCACAAATTTGTATGGTGAT 1560
Db 1501 ATTTACACTCTTGAATCTCAATGTAGAAAATGAGGAATGCCACAAATTTGTATGGTGAT 1560
Qy 1561 AAAAGTCACCTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Db 1561 AAAAGTCACCTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 8

US-09-685-166A-107
; Sequence 107, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-107

Query Match		100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1621; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCCATGGCACTGAGGCGATCTCGGTATGAGAGTGTCCGGCTCGGCCCGGGCCCGGTT 60
DB	1	CGCCATGGCACTGAGGCGATCTCGGTATGAGAGTGTCCGGCTCGGCCCGGGCCCGGTT 60
QY	61	CTGTGCTATGCTCTGCTGACTTCGGGGCGGTGTGCTACGCTGGACCGGGCCGGCTC 120
DB	61	CTGTGCTATGCTCTGCTGACTTCGGGGCGGTGTGCTACGCTGGACCGGGCCGGCTC 120
QY	121	CCGCTACGAGCTGAGCGCTTGGCCCGGGCAAGCGCTCGTAGTCTGAGACTGAGCA 180
DB	121	CCGCTACGAGCTGAGCGCTTGGCCCGGGCAAGCGCTCGTAGTCTGAGACTGAGCA 180
QY	181	GCCGCGGGAGCGCGTGTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGAGCC 240
DB	181	GCCGCGGGAGCGCGTGTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGAGCC 240
QY	241	CTTCCGCGGGGTGCTATGAGAGAACTCCAGCTGGGCCCGAGAGATCTCGAGCGGAAA 300
DB	241	CTTCCGCGGGGTGCTATGAGAGAACTCCAGCTGGGCCCGAGAGATCTCGAGCGGAAA 300
QY	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGGTT 360
DB	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGGTT 360
QY	361	AGTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420
DB	361	AGTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420
QY	421	TGCTGAGATCCGTATGATGCTGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB	421	TGCTGAGATCCGTATGATGCTGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY	481	GTGTGCACTGGGCATTTAATGCTCTTTTGGACCGCACACGACCTGACAAAGGTCAGGT 540
DB	481	GTGTGCACTGGGCATTTAATGCTCTTTTGGACCGCACACGACCTGACAAAGGTCAGGT 540
QY	541	CATTGATGCAATATGCTGGAAGAAACAGCATATTTAAGTCTTTTCTGTGGAATACTCA 600
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QY	601	GAAATCGACTCTGCGGAGCACCTCGAGACAGACATGTTGGATGGTGGAGCACTTT 660
DB	601	GAAATCGACTCTGCGGAGCACCTCGAGACAGACATGTTGGATGGTGGAGCACTTT 660
QY	661	CTATAGCACTTACAGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
DB	661	CTATAGCACTTACAGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
QY	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGAT 780
DB	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGAT 780
QY	781	GAGCATGATGATGCGCCAGAAATGAAGAAGTTGAGATGTAATTTGCAAGAGAC 840
DB	781	GAGCATGATGATGCGCCAGAAATGAAGAAGTTGAGATGTAATTTGCAAGAGAC 840
QY	841	GAGGCGAGAGTGTGTCATCTTTTCAGCGCACAGATGCTGTGCTACCTCGGCTCTGAC 900
DB	841	GAGGCGAGAGTGTGTCATCTTTTCAGCGCACAGATGCTGTGCTACCTCGGCTCTGAC 900
QY	901	TTTTGAGGAGTGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTGTATCACCAGTGA 960
DB	901	TTTTGAGGAGTGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTGTATCACCAGTGA 960
QY	961	GGAGCAGAGCTGAGCCCGCCCTGCACTCTGTGTTTAAACACCCAGCCATCCCTTC 1020
DB	961	GGAGCAGAGCTGAGCCCGCCCTGCACTCTGTGTTTAAACACCCAGCCATCCCTTC 1020
QY	1021	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATATTTGAAGATTTGGATT 1080

DB	1021	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGATTTGGATT 1080
QY	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGGTAAA 1140
DB	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGGTAAA 1140
QY	1141	AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
DB	1141	AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
QY	1201	TAGAGTAACACATAACATTTGATGATGAGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
DB	1201	TAGAGTAACACATAACATTTGATGATGAGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
QY	1261	CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
DB	1261	CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
QY	1321	AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATAAATTTATGTT 1380
DB	1321	AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATAAATTTATGTT 1380
QY	1381	AGTTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
DB	1381	AGTTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
QY	1441	TTTTGAATGGGTTCTAGTGAAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1500
DB	1441	TTTTGAATGGGTTCTAGTGAAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1500
QY	1501	ATTTACACTCTTGAATTTCTACAAATGAGAAATGAGAAATGCCAAATTTGTTGTTGAT 1560
DB	1501	ATTTACACTCTTGAATTTCTACAAATGAGAAATGAGAAATGCCAAATTTGTTGTTGAT 1560
QY	1561	AAAAGTCAGTGGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1620
DB	1561	AAAAGTCAGTGGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1620
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DB	1621	A 1621

RESULT 9

US-09-115-453-107

; Sequence 107, Application US/09115453B

; Patent No. 6657056

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

; FILE OF INVENTION: METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C4

; CURRENT APPLICATION NUMBER: US/09/115,453B

; CURRENT FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq For Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-115-453-107

Query Match		100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1621; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCCATGGCACTGAGGCGATCTCGGTATGAGAGTGTCCGGCTCGGCCCGGGCCCGGTT 60
DB	1	CGCCATGGCACTGAGGCGATCTCGGTATGAGAGTGTCCGGCTCGGCCCGGGCCCGGTT 60
QY	61	CTGTGCTATGCTCTGCTGACTTCGGGGCGGTGTGCTACGCTGGACCGGGCCGGCTC 120

|||||
Db 61 CTGTGCTATGGTCTCGGCTGACTTCGCGGCGCGTGTGTAGCGGTGACCGGCCCGCGCTC 120
Qy 121 CCGCTACGACGTGAGCCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180
Db 121 CCGCTACGACGTGAGCCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180
Qy 181 GCCGGGGAGCGCGCGTGTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCC 240
Db 181 GCCGGGGAGCGCGCGTGTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCC 240
Qy 241 CTTCGCGCGGTGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCGACAGCGGAAAA 300
Db 241 CTTCGCGCGGTGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCGACAGCGGAAAA 300
Qy 301 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTCCCGGTT 360
Db 301 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTCCCGGTT 360
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAAATTGGCAGAAG 420
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Qy 421 TGGTGAGATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGGTGGTGGCTTAT 480
Db 421 TGGTGAGATCCGTATGCCCGCTGAATCTCTGCTGACTTTGCTGGTGGTGGCTTAT 480
Qy 481 GTGTGCACTGGGCACTTATAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGGTCAGGT 540
Db 481 GTGTGCACTGGGCACTTATAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGGTCAGGT 540
Qy 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAAGTCTTTCTGTGCGAAAACTCA 600
Db 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAAGTCTTTCTGTGCGAAAACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTTGAAGTCTGATGAATCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTTGAAGTCTGATGAATCCCAATCAGAT 780
Qy 781 GAGCATGATGATTCGCCAGAAATGAAGAAGTTTCAGATGTTATTTGCAAGAAGAC 840
Db 781 GAGCATGATGATTCGCCAGAAATGAAGAAGTTTCAGATGTTATTTGCAAGAAGAC 840
Qy 841 GAAAGCAGAGTGTGCTCAAACTTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
Db 841 GAAAGCAGAGTGTGCTCAAACTTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
Qy 901 TTTTGAGGAGTGTGTTATCATATGATCAACAAGGAAACGGGCTCGTTTATCAACAGTGA 960
Db 901 TTTTGAGGAGTGTGTTATCATATGATCAACAAGGAAACGGGCTCGTTTATCAACAGTGA 960
Qy 961 GGAGCAGACGTGAGCGCGCGCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGACGTGAGCGCGCGCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTTCAAAAGGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
Db 1021 TTTTCAAAAGGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
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Db 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATACTGCTATTACAGTG 1200
|||||

Db 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATACTGCAATTACAGTG 1200
Qy 1201 TAGAGTAAACATAAACATTTGTATGTCATGGAACAATGAGGAAACAGTATTAACGTGCTTA 1260
Db 1201 TAGAGTAAACATAAACATTTGTATGTCATGGAACAATGAGGAAACAGTATTAACGTGCTTA 1260
Qy 1261 CCAGTCTAAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
Db 1261 CCAGTCTAAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTATACTAAATTTATGGT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTATACTAAATTTATGGT 1380
Qy 1381 AGTTATTTCTGCTTCCAGTTTGGTGTATATATTTGTTGATATTAAGATTTCTTGACTTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTGGTGTATATATTTGTTGATATTAAGATTTCTTGACTTTATA 1440
Qy 1441 TTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTGAT 1560
Db 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTGAT 1560
Qy 1561 AAAAGTCAGTGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
Db 1561 AAAAGTCAGTGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 10

US-09-688-489-107
; Sequence 107, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGGCACTGCAGGGCATCTCGGTTCATGGAGCTCTCGGCTGGCCCGGCCCGCTT 60
Db 1 CGCCATGGCACTGCAGGGCATCTCGGTTCATGGAGCTCTCGGCTGGCCCGGCCCGCTT 60
Qy 61 CTGTGCTATGCTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTC 120
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Db 121 CCGCTACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 180
Qy 181 GCCCGGGGAGCCCGCGTGTCTGCGGCTCTGTGCAAGCGGTCGGATGTGTGCTGGAGCC 240

181	Db		GC	CGCGGGAG	CCGCGTGTCTGGCGCGTCTGTGCAAGCGGT	CGGATGTGCTGCTGGAGCC	240
241	Qy		CTT	CCGCGCGGTGT	CATGAGAGAAATCTCAGCTGGGCC	CCAGAGATTCTGCAGCGGGA	300
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301	Qy		TCCA	GGCTTTATTTATG	CCAGGCTGAGTGGATTGGCCAGT	CAAGGCTTCTGCCGGTT	360
301	Db		TCCA	GGCTTTATTTATG	CCAGGCTGAGTGGATTGGCCAGT	CAAGGCTTCTGCCGGTT	360
361	Qy		AGCT	GGCCACGATATCA	ACTATTTTGGCTTTGT	CAGGTGTTCTCTCAAAAATTTGCAGAG	420
361	Db		AGCT	GGCCACGATATCA	ACTATTTTGGCTTTGT	CAGGTGTTCTCTCAAAAATTTGCAGAG	420
421	Qy		TG	GTGAGAAATCCG	TATGTCCTGGCTGAACTTTGCTGGT	GACTTTGCTGGTGGTGGCTTTAT	480
421	Db		TG	GTGAGAAATCCG	TATGTCCTGGCTGAACTTTGCTGGT	GACTTTGCTGGTGGTGGCTTTAT	480
481	Qy		GT	GTGCACTGGG	CATTATTAATGGCTCTTTTGTGACCG	CAACGCACTGCAAGGGT	540
481	Db		GT	GTGCACTGGG	CATTATTAATGGCTCTTTTGTGACCG	CAACGCACTGCAAGGGT	540
541	Qy		CATT	TGATGCAAAATAT	GGTGGAGAAACAGCATATTTAA	GTCTTTCTGTGGAAAACTCA	600
541	Db		CATT	TGATGCAAAATAT	GGTGGAGAAACAGCATATTTAA	GTCTTTCTGTGGAAAACTCA	600
601	Qy		GAA	ATCGAGTCTGTGG	AAGCACTCTGAGACAGAAATG	TCGTGGTGGACACCTTT	660
601	Db		GAA	ATCGAGTCTGTGG	AAGCACTCTGAGACAGAAATG	TCGTGGTGGACACCTTT	660
661	Qy		CTAT	ACGACTTACAGG	ACAGATGGGAAATCATGGCTGTGG	AGCAATAGAACCCCA	720
661	Db		CTAT	ACGACTTACAGG	ACAGATGGGAAATCATGGCTGTGG	AGCAATAGAACCCCA	720
721	Qy		GTTCT	ACGAGCTGCTG	ATCAAGGACTTGCACTTAAAGTCT	GTAGTAACTTCCCAATCAGAT	780
721	Db		GTTCT	ACGAGCTGCTG	ATCAAGGACTTGCACTTAAAGTCT	GTAGTAACTTCCCAATCAGAT	780
781	Qy		GAG	CATGGATGATTTG	CCAGCAAAATGAGAGAAAGTTG	CAGATGTTTCCAAAGAGAC	840
781	Db		GAG	CATGGATGATTTG	CCAGCAAAATGAGAGAAAGTTG	CAGATGTTTCCAAAGAGAC	840
841	Qy		GA	AGGCAGAGTGTGT	CAAAATCTTTGACGGCACAGATG	CCCTGTGTGACTCCGGTCTTGAC	900
841	Db		GA	AGGCAGAGTGTGT	CAAAATCTTTGACGGCACAGATG	CCCTGTGTGACTCCGGTCTTGAC	900
901	Qy		TTTT	TGAGGAGGTTT	TTTCATCATGATCAACAAGGAA	CGGGCTCGTTTATCAACCAGTGA	960
901	Db		TTTT	TGAGGAGGTTT	TTTCATCATGATCAACAAGGAA	CGGGCTCGTTTATCAACCAGTGA	960
961	Qy		GG	AGCAGGACGTG	AGCCCGCCCTGCACTCTGCTGTT	AAAAACCCCGACGATCCCTTC	1020
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1021	Qy		TTT	CAAAAGGATCTCT	TTTCATAGGAGAAACACTTG	AGGAGATCTTGAAGAAATTTGGATT	1080
1021	Db		TTT	CAAAAGGATCTCT	TTTCATAGGAGAAACACTTG	AGGAGATCTTGAAGAAATTTGGATT	1080
1081	Qy		CAG	CCGCGAAGAGAT	TTTATCAGCTTAACTCAGATA	AAAAATCAITTCAAAGTAAATAGGTAAA	1140
1081	Db		CAG	CCGCGAAGAGAT	TTTATCAGCTTAACTCAGATA	AAAAATCAITTCAAAGTAAATAGGTAAA	1140
1141	Qy		AG	CTAGTCTCTAA	CTTCAGGCCCA	CGGCTCAAGTGAATTTGAAATCTGATTTACAGTG	1200
1141	Db		AG	CTAGTCTCTAA	CTTCAGGCCCA	CGGCTCAAGTGAATTTGAAATCTGATTTACAGTG	1200
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1201	Db		TAG	AGTAAACATAA	CACTTCTATGCAATGGA	AAACATGGAGAAACAGTATTTACAGTGTCCCTA	1260
1261	Qy		CCA	CTCTAAATCA	AGAAAAAGATTTACAGACTCT	GTATTTCTACAGTGATGATTTGAATTTCTAAA	1320

RESULT 11

US-09-679-426-107

US-09-073-420-107
; Sequence 107, Application US/09679426

; Patent No. 6759515

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqi

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R

; APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick
APPLICANT: i: c: 1

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; APPLICANT: L1, Samuel
: APPLICANT: Wang Aijun

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; APPLICANT: Wang, Aljun
: APPLICANT: Skaiky, Yag

APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henler, William

APPLICANT: HEPLEY, WILLIAM
TITLE OF INVENTION: COMPOS

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20

FILE REFERENCE: Z10121.42/C20
CURRENT APPLICATION NUMBER: US/09/679,426

; CURRENT AFFILIATION NUMBER: 0570
; CURRENT FILING DATE: 2000-10-02

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; CURRENT FILING DATE: 2000
; NUMBER OF SEQ ID NOS: 895

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; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-679-426-107

Query Match

Query Match	100.0%;	Score 18217
Best Local Similarity	100.0%;	Pred. No. 0;

Best local similarity 100.0%, rec. no. 0;
Matches 1621: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1. **Introduction**

1 CGCCATGGCACTGCAGGGCATCTCGGTTCATGGAGCTGTCCGGCCCTGGCCCCGGCCCGTT 60

Db 1 CGCCATGGCACTGCAGGGCATCTCGGTATGGAGCTGTCCGGCTGGCCCCGGCCCGTT 60

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QY 121 CCGTACGACGTGAGCCGCTTTGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180
Db 121 CCGTACGACGTGAGCCGCTTTGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180
QY 181 GCCCGGGAGCGCGGCTGCGGCGTCTGTGCAAGCGGTGCGATGCTGTGGAGCC 240
Db 181 GCCCGGGAGCGCGGCTGCGGCGTCTGTGCAAGCGGTGCGATGCTGTGGAGCC 240
QY 241 CTTCCGCGCGGTGTGATGAGAAATCTCCAGCTGGGCCAGAGATTTCTGACGCGGAAA 300
Db 241 CTTCCGCGCGGTGTGATGAGAAATCTCCAGCTGGGCCAGAGATTTCTGACGCGGAAA 300
QY 301 TCCAAAGGCTTATTTATGACAGCTGAGTGAATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360
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QY 960 TTTTCAGGAGTGTGTTTCATGATGATCAAAAGGAGCGGCTCGTTTATCACCAGTGA 960
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Db 1021 TTTTAAAGGGATTCCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGATTTGGATT 1080
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Db 1621 A 1621
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RESULT 12

US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. 6800746

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCATGGCACTGCAGGGCATCTCGGTGATGGAGCTGTCCGGCTGCGCCCGGCGCGCTT 60

Db 1 CGCCATGGCACTGCGGGCATCTCGTTCATGAGCTGTCGGCCCTGGCCCGGGCCGTT 60
Qy 61 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCGCGCTC 120
Db 61 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGGTGTGGTACCGGTGGACCGCGCGCTC 120
Qy 121 CGCTACGACGTGAGCGGCTTCGGGGCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180
Db 121 CGCTACGACGTGAGCGGCTTCGGGGCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180
Qy 181 GCGCGGGGAGCGCGGCTCTCGGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGGCC 240
Db 181 GCGCGGGGAGCGCGGCTCTCGGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGGCC 240
Qy 241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCCGAGAGATTCGACGGGGAAA 300
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Db 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTT 360
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Db 661 CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
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Db 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780
Qy 781 GAGCATGATGATTTGCCGCAAAATGAAGAAAGTTTGGATGATTTTGGAAAGAGAC 840
Db 781 GAGCATGATGATTTGCCGCAAAATGAAGAAAGTTTGGATGATTTTGGAAAGAGAC 840
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Db 841 GAAGCAGATGCTGCTCAAACTTTTGGCGGACAGATGCTGTGAGCTCCGGTCTGAC 900
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Db 901 TTTTTCAGGAGGTGTTTCATCATGATCAAAAGGAACGGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGGAGCTGAGCGCCCGCTGACCTCTGTGTTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGGAGCTGAGCGCCCGCTGACCTCTGTGTTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTTCAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAGATTTGGATT 1080
Db 1021 TTTTCAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAGATTTGGATT 1080
Qy 1081 CAGCCGCAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAAATAGGTTAA 1140

Db 1081 CAGCCGCAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAAATAGGTTAA 1140
Qy 1141 AGCTAGTCTCTAACTTCAGGCCCAAGCTCAAGTGAATTTGAAATCTGCTGATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCAGGCCCAAGCTCAAGTGAATTTGAAATCTGCTGATTTACAGTG 1200
Qy 1201 TAGAGTAAACATTAACATTTGATGATGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Db 1201 TAGAGTAAACATTAACATTTGATGATGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1320
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Db 1501 ATTTACACTCTGATTTCTACAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1560
Qy 1561 AAAAGTCACTGAAACAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1620
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Db 1621 A 1621

RESULT 13

US-09-651-236-107

; Sequence 107, Application US/09651236

; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651.236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-107

Query Match		100.0%;	Score 1621;	DB 3;	Length 1621;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1621;		Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	CGCCATGSCACTGAGGGCATCTCGGTCAATGAGCTGTCGGCCCTCGGCCCGGGCCCGTT	60			
Db	1	CGCCATGGCACTGAGGGCATCTCGGTCAATGAGCTGTCGGCCCTCGGCCCGGGCCCGTT	60			
Qy	61	CTGTGCTATGTCCTGCGTGAATCTTGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTC	120			
Db	61	CTGTGCTATGTCCTGCGTGAATCTTGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTC	120			
Qy	121	CCGCTACACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGACGCTGGACCTGAAGCA	180			
Db	121	CCGCTACACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGACGCTGGACCTGAAGCA	180			
Qy	181	CCCGGGGAGCCGCGTCTGCGCGCTCTGTCAAGCGGTCGATGTCGTGGAGCC	240			
Db	181	CCCGGGGAGCCGCGTCTGCGCGCTCTGTCAAGCGGTCGATGTCGTGGAGCC	240			
Qy	241	CTTCGCGCGCGTGTGTCAGGAACTCCAGCTGGGCCCGAGAGATTCCTGCAAGCGGAA	300			
Db	241	CTTCGCGCGCGTGTGTCAGGAACTCCAGCTGGGCCCGAGAGATTCCTGCAAGCGGAA	300			
Qy	301	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360			
Db	301	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360			
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTGTGCAAGCTGTCGCAAAATGGCAGAG	420			
Db	361	AGCTGGCCACGATATCAACTATTTGGCTTGTGCAAGCTGTCGCAAAATGGCAGAG	420			
Qy	421	TGGTGAGAAATCCGATGCGCCGCTGAATCTCTGCTGACTTTGCTGGTGGCTTAT	480			
Db	421	TGGTGAGAAATCCGATGCGCCGCTGAATCTCTGCTGACTTTGCTGGTGGCTTAT	480			
Qy	481	GTGTGACTGGGCATTAATAGGCTCTTTTGAACGCAACGCACTGACAGGGTCAGGT	540			
Db	481	GTGTGACTGGGCATTAATAGGCTCTTTTGAACGCAACGCACTGACAGGGTCAGGT	540			
Qy	541	CATTGATCAAAATGTTGGAGGAAAGCAAGATATTTAAGTCTTTCTGTGCAAACTCA	600			
Db	541	CATTGATCAAAATGTTGGAGGAAAGCAAGATATTTAAGTCTTTCTGTGCAAACTCA	600			
Qy	601	GAATTCGAGTCTGTGGGAGCACTTCGAGGACAGAACTTGTGGATGGTGAGCACCTTT	660			
Db	601	GAATTCGAGTCTGTGGGAGCACTTCGAGGACAGAACTTGTGGATGGTGAGCACCTTT	660			
Qy	661	CTATACGCTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720			
Db	661	CTATACGCTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720			
Qy	721	GTTCCTACGAGTGTGATCAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGAT	780			
Db	721	GTTCCTACGAGTGTGATCAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGAT	780			
Qy	781	GAGCATGATGATTCGCCAGAAATGAAGAAGTTTTCAGATGATTTTGAAGAAGAC	840			
Db	781	GAGCATGATGATTCGCCAGAAATGAAGAAGTTTTCAGATGATTTTGAAGAAGAC	840			
Qy	841	GAAGCAGAGTGTGTCAAATCTTTTGAACGCAAGATCCCTGTGTGATCCGGTTCTGAC	900			
Db	841	GAAGCAGAGTGTGTCAAATCTTTTGAACGCAAGATCCCTGTGTGATCCGGTTCTGAC	900			
Qy	901	TTTTGAGAGGTTTTCATGATCAACAAGGAGCGGGCTCGTTTATCACAGTGA	960			
Db	901	TTTTGAGAGGTTTTCATGATCAACAAGGAGCGGGCTCGTTTATCACAGTGA	960			
Qy	961	GGAGCAGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1020			
Db	961	GGAGCAGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1020			

Qy	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTCAAGAAATTTGATT	1080			
Db	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTCAAGAAATTTGATT	1080			
Qy	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAITGAAAGTAAATAGGTAAA	1140			
Db	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAITGAAAGTAAATAGGTAAA	1140			
Qy	1141	AGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATCTGATTTACAGTG	1200			
Db	1141	AGCTAGTCTCTAACTCCAGGCCACCGCTCAAGTGAATTTGAATCTGATTTACAGTG	1200			
Qy	1201	TAGAGTAAACATAAATCTGATGCGTGAATAATGATGCGTGAATAATGATGCTGCTA	1260			
Db	1201	TAGAGTAAACATAAATCTGATGCGTGAATAATGATGCGTGAATAATGATGCTGCTA	1260			
Qy	1261	CCACTCTAACTCAAGAAAGAAATTTACAGACTCTGATTTCTCAGTGATGATTTCTAAA	1320			
Db	1261	CCACTCTAACTCAAGAAAGAAATTTACAGACTCTGATTTCTCAGTGATGATTTCTAAA	1320			
Qy	1321	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATGGT	1380			
Db	1321	AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATGGT	1380			
Qy	1381	AGTTATTCCTGCTTCCAGTTTGTGATATATTTGTTGATTTAAGATTTCTTGACTTATA	1440			
Db	1381	AGTTATTCCTGCTTCCAGTTTGTGATATATTTGTTGATTTAAGATTTCTTGACTTATA	1440			
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Db	1441	TTTTGAATGGTCTTAGTGAAAGAAATGATATTTCTTTGAAGACATCGATATACATTT	1500			
Qy	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTAT	1560			
Db	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTAT	1560			
Qy	1561	AAAGTCACTGAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAA	1620			
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Db	1621	A 1621				

RESULT 14

US-09-030-606-107
; Sequence 107, Application US/09030606
; Patent No. 6887660
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.428C3

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 1621 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-030-606-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCCATGGCACTGCAGGGCATCTCGGTTCATGGAGCTGTCGGGCTGGCCCGGGCCGGT 60

QY 61 CTGTGCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCGCTC 120
DB 61 CTGTGCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCGCTC 120

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DB 121 CGCTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTGCTAGTGTGGACCTGAAGCA 180

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DB 181 GCGCGGGGAGCGCGGTCTGCGGCGTCTGTGCAAGCGGTGGATGCTGCTGGAGCC 240

QY 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGAAA 300
DB 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGAAA 300

QY 301 TCGAGGCTATTATGCGAGGCTGAGTGGATTTGGCCAGTCAGAGCTTCTGCGGGT 360
DB 301 TCGAGGCTATTATGCGAGGCTGAGTGGATTTGGCCAGTCAGAGCTTCTGCGGGT 360

QY 361 AGTGGCCACGATATCAACTATTGGCTTTGTCAGGTGTTCTCAAAATTTGGCAGAG 420
DB 361 AGTGGCCACGATATCAACTATTGGCTTTGTCAGGTGTTCTCAAAATTTGGCAGAG 420

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DB 421 TGGTGAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTAT 480

QY 481 GTGTGCACTGGGCAATTATATGGCTCTTTTGAACGCAACGCACTGCAAGGGTCAGT 540
DB 481 GTGTGCACTGGGCAATTATATGGCTCTTTTGAACGCAACGCACTGCAAGGGTCAGT 540

QY 541 CATTCATGCAATATGTTGGAGGACAGCATATTAAAGTCTTTCTGTCGAAACTCA 600
DB 541 CATTCATGCAATATGTTGGAGGACAGCATATTAAAGTCTTTCTGTCGAAACTCA 600

QY 601 GAAATCGAGTCTGTGGAGAGCACCTCGAGCAAGAACTGTTGGATGGTGGAGCACTTT 660
DB 601 GAAATCGAGTCTGTGGAGAGCACCTCGAGCAAGAACTGTTGGATGGTGGAGCACTTT 660

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DB 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGACTTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGACTTCCCAATCAGAT 780

QY 781 GAGCATGGATGTTGGCCAGAAATGAAGAAGTTTGCAGATGATTGTCAGAAAGAC 840

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DB 781 GAGCATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGATTGTCAGAAAGAC 840
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DB 841 GAAGGCAGAGTGGTGTCAAACTTTTGACGGCACAGATGCTCTGTGTGACTCCGGTCTGAC 900
QY 901 TTTTGAGGAGTGTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
DB 901 TTTTGAGGAGTGTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
QY 961 GGAGCAGAGCTGAGCGCCCGCTGACCTCTGCTGTGTTAAACACCCGACCATCCCTTC 1020
DB 961 GGAGCAGAGCTGAGCGCCCGCTGACCTCTGCTGTGTTAAACACCCGACCATCCCTTC 1020
QY 1021 TTTTAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGTACTTTGAAGAAATTTGGATT 1080
DB 1021 TTTTAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGTACTTTGAAGAAATTTGGATT 1080
QY 1081 CAGCCGCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGATAA 1140
DB 1081 CAGCCGCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGATAA 1140
QY 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGCTCAAGTGAATTTGAATATCTGCAATTTACAGTG 1200
DB 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGCTCAAGTGAATTTGAATATCTGCAATTTACAGTG 1200
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DB 1201 TAGAGTAACACATAACATTGTATGATGGAACATGGAGGACAGTATTACAGTGTCTTA 1260
QY 1261 CCACCTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
DB 1261 CCACCTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
QY 1321 AATGGTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATACTAAATTTATGTT 1380
DB 1321 AATGGTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATACTAAATTTATGTT 1380
QY 1381 AGTTATTTCTGCTTCCAGTCTTGTGATATTTGCTGATATTTGCTGATATTAAGATTTCTTGACTATA 1440
DB 1381 AGTTATTTCTGCTTCCAGTCTTGTGATATTTGCTGATATTTGCTGATATTAAGATTTCTTGACTATA 1440
QY 1441 TTTTCAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTGAAAGACATCGATATACATTT 1500
DB 1441 TTTTCAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTGAAAGACATCGATATACATTT 1500
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DB 1501 ATTTACACTCTGATTTCTACAAATGTAGAAAATGAGGAAATGCCAATAATTTGATGGTGAT 1560
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DB 1561 AAAAGTCACTGAAACAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
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RESULT 15

US-09-657-279-107

; Sequence 107, Application US/09657279

; Patent No. 6894146

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:22:01 ; Search time 2581.16 Seconds
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7716.790 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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21	1574.2	97.1	2005	3	US-09-967-305-1
22	1574.2	97.1	2005	3	US-09-967-305-10
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24	1574.2	97.1	2005	10	US-10-909-035-104
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26	1574.2	97.1	2069	6	US-10-205-823-17
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31	1524.8	94.1	2068	10	US-10-756-149-1746
32	1245.4	76.8	2946	6	US-10-205-823-29
33	1245.4	76.8	2946	8	US-10-316-540-13
34	1245.4	76.8	2946	13	US-11-051-454-29
35	1243.8	76.7	3023	3	US-09-967-305-8
36	1243.8	76.7	3023	6	US-10-205-823-21
37	1243.8	76.7	3023	13	US-11-051-454-21
38	1142.8	70.5	1146	3	US-09-967-305-3
39	1134.4	70.0	2626	6	US-10-205-823-27
40	1134.4	70.0	2626	13	US-11-051-454-27
41	1132.8	69.9	3654	3	US-09-967-305-6
42	1132.8	69.9	3654	6	US-10-205-823-19
43	1132.8	69.9	3654	13	US-11-051-454-19
44	1132.8	69.9	3654	16	US-11-203-526-5
45	940	58.0	1039	8	US-10-378-029-3

ALIGNMENTS

RESULT 1

US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. US200202248A1

GENERAL INFORMATION:

; APPLICANT: Xu Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGGCATCTCGTTCATGGAGCTGTCGGCCTGGCCCGGCCGCGT 60

Db 1 CGCCATGGCACTCGAGGCGATCTGGTCTATGGAGCTGTCCGCGCTTGGCCCCGGGCGCGTT 60
Qy 61 CTGTGCTATGCTCTCGGTGCTGCTTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCCGGCTC 120
Db 61 CTGTGCTATGCTCTCGGTGCTGCTTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCCGGCTC 120
Qy 121 CGGTACGAGCTGAGCGCGCTTGGGCGGCGGCAAGGCTCGCTAGTGTGGACCTGAAGCA 180
Db 121 CGGTACGAGCTGAGCGCGCTTGGGCGGCGGCAAGGCTCGCTAGTGTGGACCTGAAGCA 180
Qy 181 GCGCGGGGAGCGCGCGTGTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240
Db 181 GCGCGGGGAGCGCGCGTGTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240
Qy 241 CTTCCGCGCGGTGTGTCAGGAGAACTCCAGCTGGGCGCCAGAGATTCCTGACGCGGAAAA 300
Db 241 CTTCCGCGCGGTGTGTCAGGAGAACTCCAGCTGGGCGCCAGAGATTCCTGACGCGGAAAA 300
Qy 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGCTCAGGAAGCTCTCGCGGTT 360
Db 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTTGGCCAGCTCAGGAAGCTCTCGCGGTT 360
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATTGCGAGAG 420
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATTGCGAGAG 420
Qy 421 TGGTGAGAAATCCGTATGCGCGCGTGAATCTCCTCGGCTGACTTGTGGTGGTGGCTTTAT 480
Db 421 TGGTGAGAAATCCGTATGCGCGCGTGAATCTCCTCGGCTGACTTGTGGTGGTGGCTTTAT 480
Qy 481 GTGTGCACTGGGCATTAATAGGCTCTTTTGAACCGCAACGCACTGACAGGGTTCAGGT 540
Db 481 GTGTGCACTGGGCATTAATAGGCTCTTTTGAACCGCAACGCACTGACAGGGTTCAGGT 540
Qy 541 CATTGATCCAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCA 600
Db 541 CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCA 600
Qy 601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTGTTGGATGGTGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTGTTGGATGGTGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGCGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
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Db 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGAC 840
Qy 841 GAAGCAGAGTGGTTCAAAATCTTTGACGGCACAGATGCTGTGAGACTCCGGTTCTGAC 900
Db 841 GAAGCAGAGTGGTTCAAAATCTTTGACGGCACAGATGCTGTGAGACTCCGGTTCTGAC 900
Qy 901 TTTTTCAGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTTCAGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGACGTGAGCGCGCGCTCGACCTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020
Db 961 GGAGCAGACGTGAGCGCGCGCTCGACCTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020
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Db 1021 TTTTAAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCGCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140

Db 1081 CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCTATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCTATTTACAGTG 1200
Qy 1201 TAGAGTAAACATAAACATTTGATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Db 1201 TAGAGTAAACATAAACATTTGATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Qy 1261 CCACTCTAAATCAAGAAAGAAATTAACAGACTCTGATTTACAGTGAATTTGAATTTCTAAA 1320
Db 1261 CCACTCTAAATCAAGAAAGAAATTAACAGACTCTGATTTACAGTGAATTTGAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGCTTTTGTATTTATAAACTTTGGGTACTTATACTAAATTTATGGT 1380
Db 1321 AATGGTTATCATTTAGGCTTTTGTATTTATAAACTTTGGGTACTTATACTAAATTTATGGT 1380
Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTCTTGACTTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTCTTGACTTTATA 1440
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTGATTTCTACAATGTAGAAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1560
Db 1501 ATTTACACTCTGATTTCTACAATGTAGAAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1560
Qy 1561 AAAAGTCACGTGAAACAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAA 1620
Db 1561 AAAAGTCACGTGAAACAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 2

US-09-780-669-107
; Sequence 107, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621


```
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CGCATGGCACTGCGAGGCACTCTGGTCAATGGAGCTGTCCGGCTTGGCCCGCCGCGCGTT  60
Db      1  CGCATGGCACTGCGAGGCACTCTGGTCAATGGAGCTGTCCGGCTTGGCCCGCCGCGCGTT  60

Qy     61  CTGTGCTATGTCCTGGCTGACTTTCGGGGCGCGTGTGGTACCGCGTGGACCGCCCGCGTC  120
Db     61  CTGTGCTATGTCCTGGCTGACTTTCGGGGCGCGTGTGGTACCGCGTGGACCGCCCGCGTC  120

Qy    121  CCGTACGACGTAGCCCTTGGCGCGCTGTGCAAGCGGTCCGATGCTGCTGGACCTGGAAGCA  180
Db    121  CCGTACGACGTAGCCCTTGGCGCGCTGTGCAAGCGGTCCGATGCTGCTGGACCTGGAAGCA  180

Qy    181  GCCGGGGAGCGCGCTGTGCGCGCTGTGCAAGCGGTCCGATGCTGCTGGAGCC  240
Db    181  GCCGGGGAGCGCGCTGTGCGCGCTGTGCAAGCGGTCCGATGCTGCTGGAGCC  240

Qy    241  CTTCCGCGCGGTGTGTCGAGAACTCCAGTGGGCGCCAGAGATTTCTGACGCGGAAAA  300
Db    241  CTTCCGCGCGGTGTGTCGAGAACTCCAGTGGGCGCCAGAGATTTCTGACGCGGAAAA  300

Qy    301  TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAGCTTCTGCCGTT  360
Db    301  TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAGCTTCTGCCGTT  360

Qy    361  AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAG  420
Db    361  AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAG  420

Qy    421  TGGTGAGAAATCCGTATGCCCGCTGAAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT  480
Db    421  TGGTGAGAAATCCGTATGCCCGCTGAAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT  480

Qy    481  GTGTGCACTGGGCATTTAATGGCTCTTTTGGACCGGACAGCATATTTAAGTCTTCTG  540
Db    481  GTGTGCACTGGGCATTTAATGGCTCTTTTGGACCGGACAGCATATTTAAGTCTTCTG  540

Qy    541  CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAGTCTTCTGCTGGAAACTCA  600
Db    541  CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAGTCTTCTGCTGGAAACTCA  600

Qy    601  GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTGTTGGATGGTGAGCACCTTT  660
Db    601  GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTGTTGGATGGTGAGCACCTTT  660

Qy    661  CTATACGACTTACAGGACAGCGATGGGGAATTCATGGCTGTGGAGCAATAGACCCCA  720
Db    661  CTATACGACTTACAGGACAGCGATGGGGAATTCATGGCTGTGGAGCAATAGACCCCA  720

Qy    721  GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT  780
Db    721  GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT  780
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RESULT 4

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US-09-822-827-107
; Sequence 107, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
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Qy      781  GAGCATGATGATTGGCCCAAAATGAAGAAGAGTTTGCAGATGTATTTCAAAGAAGAC  840
Db      781  GAGCATGATGATTGGCCCAAAATGAAGAAGAGTTTGCAGATGTATTTCAAAGAAGAC  840

Qy     841  GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC  900
Db     841  GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC  900

Qy     901  TTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA  960
Db     901  TTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA  960

Qy     961  GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC  1020
Db     961  GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC  1020

Qy    1021  TTTTCAAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATT  1080
Db    1021  TTTTCAAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATT  1080

Qy    1081  CAGCCGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAAAGGTAAA  1140
Db    1081  CAGCCGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAAAGGTAAA  1140

Qy    1141  AGCTAGTCTCTAACTTCCAGGCCCGCCCGCTCAAGTGAATTTGATCTGCAATTTACAGTG  1200
Db    1141  AGCTAGTCTCTAACTTCCAGGCCCGCCCGCTCAAGTGAATTTGATCTGCAATTTACAGTG  1200

Qy    1201  TAGAGTAAACATAACTTGTATGTCATGGAACCATGAGGAAACAGATATTACAGTGTCTTA  1260
Db    1201  TAGAGTAAACATAACTTGTATGTCATGGAACCATGAGGAAACAGATATTACAGTGTCTTA  1260

Qy    1261  CCACTCTAAATCAAGAAAGAAATTACAGACTCTGATTCTACAGTGAATGAATTTCTAAA  1320
Db    1261  CCACTCTAAATCAAGAAAGAAATTACAGACTCTGATTCTACAGTGAATGAATTTCTAAA  1320

Qy    1321  AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTACTTATACTAAATTTATGGT  1380
Db    1321  AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTACTTATACTAAATTTATGGT  1380

Qy    1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTTCTGACTTATA  1440
Db    1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAAGATTTCTGACTTATA  1440

Qy    1441  TTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTTGAAGACATCGATATACATTT  1500
Db    1441  TTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTTGAAGACATCGATATACATTT  1500

Qy    1501  ATTTACACTCTTGATTTCTACAAATGAGAAATGAGGAAATGCCACAAATTTGATGGTGAT  1560
Db    1501  ATTTACACTCTTGATTTCTACAAATGAGGAAATGAGGAAATGCCACAAATTTGATGGTGAT  1560

Qy    1561  AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAA  1620
Db    1561  AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAA  1620

Qy    1621  A 1621
Db    1621  A 1621
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; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; -09-822-827-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGCGACTGACGGGCATCTCGGTCAATGAGCTGTCCGGCTCGCCCGCCGGCCGTT 60
DB 1 CGCCATGCGACTGACGGGCATCTCGGTCAATGAGCTGTCCGGCTCGCCCGCCGGCCGTT 60

QY 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 CCCTACGAGCTGAGCGCGCTTGGGCGGCGGCAAGCGCTCGCTAGTGTGCTGAGCA 180
DB 121 CCCTACGAGCTGAGCGCGCTTGGGCGGCGGCAAGCGCTCGCTAGTGTGCTGAGCA 180

QY 181 GCCGCGGGAGCGCGCTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240
DB 181 GCCGCGGGAGCGCGCTGCTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240

QY 241 CTTCCGCGCGGTGTGATGAGAGAACTCCAGCTGGGCGGCAAGATTCGAGCGGGA 300
DB 241 CTTCCGCGCGGTGTGATGAGAGAACTCCAGCTGGGCGGCAAGATTCGAGCGGGA 300

QY 301 TCCAAGGCTATTATGTCAGGCTGAGTGATTTGGCAGTCAAGAGCTTCTGCGCGGT 360
DB 301 TCCAAGGCTATTATGTCAGGCTGAGTGATTTGGCAGTCAAGAGCTTCTGCGCGGT 360

QY 361 AGCTGCGCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAAATTCGAGAG 420
DB 361 AGCTGCGCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAAATTCGAGAG 420

QY 421 TGTGAGAAATCCGTATGCCCCGTGATCTCCCTGCGTGAATTTGCTGGTGGTGGCTTAT 480
DB 421 TGTGAGAAATCCGTATGCCCCGTGATCTCCCTGCGTGAATTTGCTGGTGGTGGCTTAT 480

QY 481 GTCTGCACTGGGCAATTAATGCTCTTTTGGCCGACAGCTGCAAGGCTCAGGT 540
DB 481 GTCTGCACTGGGCAATTAATGCTCTTTTGGCCGACAGCTGCAAGGCTCAGGT 540

QY 541 CATTTGATGCAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGA 600
DB 541 CATTTGATGCAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGA 600

QY 601 GAAATCAGTCTGTGGAGGACACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660
DB 601 GAAATCAGTCTGTGGAGGACACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660

QY 661 CTATACAGCTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGACCCCA 720
DB 661 CTATACAGCTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGACCCCA 720

QY 721 GTTCTACGAGCTGTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGTGATCAAGAGCTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780

QY 781 GAGCATGGATGATTGGCCAGAAATGAAGAGAGTTTGCAGATGTATTTGCAAGAGAC 840
DB 781 GAGCATGGATGATTGGCCAGAAATGAAGAGAGTTTGCAGATGTATTTGCAAGAGAC 840

QY 841 GAAGGACAGTGTGTCAATCTTTGACGACAGATGCTGTGACTCCGCTTCTGAC 900
DB 841 GAAGGACAGTGTGTCAATCTTTGACGACAGATGCTGTGACTCCGCTTCTGAC 900

QY 901 TTTTGAGGAGTTGTTTCATCATGATCACAAAGGAAACGGGGCTGCTTTTATCACCAGTGA 960
DB 901 TTTTGAGGAGTTGTTTCATCATGATCACAAAGGAAACGGGGCTGCTTTTATCACCAGTGA 960
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RESULT 5

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US-09-115-453-107
; Sequence 107, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-115-453-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
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Best Local Similarity 100.0%; Pred. No. 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	CGCCATGGCACTGCAGGGCATCTCGGTCA	TGAGAGCTGTCCGGCTGTGGCCCGGGCCGGT	60					
Qy	61	CTGTGCTATGGTCC	TGTGGCTCACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTC	120					
Db	61	CTGTGCTATGGTCC	TGTGGCTCACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTC	120					
Qy	121	CCGCTACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTCTGACCTGGAAGCA	180						
Db	121	CCGCTACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTCTGACCTGGAAGCA	180						
Qy	181	GCSCGGGAGCGCCGCTGTCTGGCGCTCTGTGTCAAGCGTCCGATGTGCTGTCTGGAGCC	240						
Db	181	GCSCGGGAGCGCCGCTGTCTGGCGCTCTGTGTCAAGCGTCCGATGTGCTGTCTGGAGCC	240						
Qy	241	CTTTCGCCCGCGGTGTCA	TGGAGAAATCCAGCTGGGCCCAAGAGATTCTGCAGCGGGAAAA	300					
Db	241	CTTTCGCCCGCGGTGTCA	TGGAGAAATCCAGCTGGGCCCAAGAGATTCTGCAGCGGGAAAA	300					
Qy	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTACAGGAAGCTTCTGCCGCTT	360						
Db	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTACAGGAAGCTTCTGCCGCTT	360						
Qy	361	AGCTGGCCACGATCAACTATTATTTGGCTTTGTCTCAGGTGTTCTCTCAAAAATTCGCAAG	420						
Db	361	AGCTGGCCACGATCAACTATTATTTGGCTTTGTCTCAGGTGTTCTCTCAAAAATTCGCAAG	420						
Qy	421	TGGTGAAGATCCGCTATGCCCGCTGAAATCTCTGGCTGACTTTTGTCTGGTGGCTTAT	480						
Db	421	TGGTGAAGATCCGCTATGCCCGCTGAAATCTCTGGCTGACTTTTGTCTGGTGGCTTAT	480						
Qy	481	GTGTGCACTGGGCAATTAATATGGCTCTTTTGTGACCGCACGCACTGCAAGGGTCAGGT	540						
Db	481	GTGTGCACTGGGCAATTAATATGGCTCTTTTGTGACCGCACGCACTGCAAGGGTCAGGT	540						
Qy	541	CATTGATGCAAAATGTGGNAGAAACAGCATATTTAAGTTCTTTCTGTGTGGAAACTCA	600						
Db	541	CATTGATGCAAAATGTGGNAGAAACAGCATATTTAAGTTCTTTCTGTGTGGAAACTCA	600						
Qy	601	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTGGATGGTGGAGCACCTTT	660						
Db	601	GAAATCGAGTCTGTGGNAGCACCTCGAGGACAGAAATGTGGATGGTGGAGCACCTTT	660						
Qy	661	CTATACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720						
Db	661	CTATACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720						
Qy	721	GTTCCTACGAGTGTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT	780						
Db	721	GTTCCTACGAGTGTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT	780						
Qy	781	GAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTTCAGATGCTATTTGCAAGAAGAC	840						
Db	781	GAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTTCAGATGCTATTTGCAAGAAGAC	840						
Qy	841	GAAGGCAGAGTGTGTCAAAATCTTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTTGAC	900						
Db	841	GAAGGCAGAGTGTGTCAAAATCTTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTTGAC	900						
Qy	901	TTTTTGAGAGGTTGTTTATCATGATCAACAAGAGAAACGGGGCTGCTTTTATCACCAGTGA	960						
Db	901	TTTTTGAGAGGTTGTTTATCATGATCAACAAGAGAAACGGGGCTGCTTTTATCACCAGTGA	960						
Qy	961	GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1020						
Db	961	GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1020						
Qy	1021	TTTTCAAAAGGGATCCCTTTTCATPAGGAGAACACACTGAGGAGATACCTTGAAGATTTGGATT	1080						

RESULT 6

RESULT 6
IIS-09-232-880-107

US-09-232-880-107
: Sequence 107. Application US/09232880; sequence 107, Application 03/03/2002
; Publication No. US20020182596A1; PUBLICATION NO: 0324
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.428C6

; CURRENT APPLICATION NUMBER: US/09/232,880

;; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

```
; SOFTWARE: FastSEQ for Windows Version 3.0
```

; SEQ ID NO 107

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; LENGTH: 1621

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; TYPE: DNA

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; ORGANISM: Homo sapien
 118 00 222-880-107

US-09-232-880-107

```
Query Match
100 0% score 1621: DB 3: Length 1621:
```

Query Match	100.0%;	score 1621;	DB 3;	length 1621;
Best Local Similarity	100.0%;	pred. No. 0;		

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621: Conservative 0: Mismatches 0: Indels 0:

1 CCCCATCGCACTGCAAGGCATCTCGGTCAATGGAGCTGTCCGCCCGGGCCCCGTT 60

QY 1 CGCCATGGGCACTGGAGGGCACTCCGGTCATGGAGCAGTCCGGCCAGGCCCGTTCGTTT

D6 1 CGCCATGGCAC^TGCGAGGCA^TC^TCGGTCA^TGGAGCTGTCGGCCCTGGCCCCCGT^T 80

Db 61 CTGTGCTATGGTCTCGCTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCGCTC 120
Qy 121 CCGCTACGAGCTGAGCGGCTTGGCCCGGGCAAGCGCTCGTAGTCTGAGCCTGAAGCA 180
Db 121 CCGCTACGAGCTGAGCGGCTTGGCCCGGGCAAGCGCTCGTAGTCTGAGCCTGAAGCA 180
Qy 181 GCGCGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCC 240
Db 181 GCGCGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCC 240
Qy 241 CTTCCCGCGGCTCATGAGAGAACTCCAGCTGGGCCAGAGATTCAGCGGGGAAAA 300
Db 241 CTTCCCGCGGCTCATGAGAGAACTCCAGCTGGGCCAGAGATTCAGCGGGGAAAA 300
Qy 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTT 360
Db 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTT 360
Qy 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAG 420
Db 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAG 420
Qy 421 TGGTGAAGATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGCTTAT 480
Db 421 TGGTGAAGATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGCTTAT 480
Qy 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGAACCGCACACGCACTGACAAAGGGTCAGGT 540
Db 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGAACCGCACACGCACTGACAAAGGGTCAGGT 540
Qy 541 CATTGATGCAATATGCTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600
Db 541 CATTGATGCAATATGCTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTGGATGGTGGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTGGATGGTGGAGCACCTTT 660
Qy 661 CTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATGAAACCCCA 720
Db 661 CTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATGAAACCCCA 720
Qy 721 GTTCTACGAGCTCTCATCAAGGACTTGAGCTTAAAGTCTGATGAACCTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTCTCATCAAGGACTTGAGCTTAAAGTCTGATGAACCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAAGAAC 840
Db 781 GAGCATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAAGAAC 840
Qy 841 GAAGGAGAGTGTGTCAAACTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
Db 841 GAAGGAGAGTGTGTCAAACTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
Qy 901 TTTTGAAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTCA 960
Db 901 TTTTGAAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTCA 960
Qy 961 GGAGCAGGAGCTGAGCGCCCGCTGACCTCTGCTGTGTTAAACACCCCGAGCCATCCCTTC 1020
Db 961 GGAGCAGGAGCTGAGCGCCCGCTGACCTCTGCTGTGTTAAACACCCCGAGCCATCCCTTC 1020
Qy 1021 TTTTCAAAAGGATCTTTTATAGGAGAAACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
Db 1021 TTTTCAAAAGGATCTTTTATAGGAGAAACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCCCGGAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAGTAAATAGGTAA 1140
Db 1081 CAGCCCGGAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAGTAAATAGGTAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCCGCTCAAGTGAATTTGAAATCTGCATTTACAGTG 1200

Db 1141 AGCTAGTCTCTAACTTCCAGGCCCGCTCAAGTGAATTTGAAATCTGCATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAACATTTGATGATGAAACATGGAGAACAGTATTTACAGTGTCCTA 1260
Db 1201 TAGAGTAACACATAACATTTGATGATGAAACATGGAGAACAGTATTTACAGTGTCCTA 1260
Qy 1261 CCACCTCTAATCAAGAAAAAATTCAGAGCTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320
Db 1261 CCACCTCTAATCAAGAAAAAATTCAGAGCTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320
Qy 1321 AATGTTATCATAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATAATTTATGTT 1380
Db 1321 AATGTTATCATAGGGCTTTTGAATTTATAAACTTTGGGTACTTATATAATTTATGTT 1380
Qy 1381 AGTATTTCTGCCCTCCAGTTTCTGATATATTTGTTGATATTTGTTGATTTAAAGATTTCTTGACTTATA 1440
Db 1381 AGTATTTCTGCCCTCCAGTTTCTGATATATTTGTTGATATTTGTTGATTTAAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGGTCTTAGTGAAAAAGAAATGATATATTTCTTGAAGCATCGATATACATTT 1500
Db 1441 TTTTGAATGGGTCTTAGTGAAAAAGAAATGATATATTTCTTGAAGCATCGATATACATTT 1500
Qy 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAAATGCCACAAATTTGATGGTAT 1560
Db 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAAATGCCACAAATTTGATGGTAT 1560
Qy 1561 AAAAGTCCAGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Db 1561 AAAAGTCCAGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 7

US-09-895-793-107
; Sequence 107, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Poy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-895-793-107

Query Match 100.0%; Score 1621; DB 3; Length 1621; Best Local Similarity 100.0%; Pred. No. 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CGCCATGGCACTGCAGGCGCATCTCGGTTCATGGAGCTGTCGGCCCTGGCCCGCGGCGCGGTT	60						
Db	1	CGCCATGGCACTGCAGGCGCATCTCGGTTCATGGAGCTGTCGGCCCTGGCCCGCGGCGCGGTT	60						
Qy	61	CTGTGCTATGGTCCTGGCTGACTTCGGGCGCGGTGTGGTAGCGGTGACCGGCGCCGGCTC	120						
Db	61	CTGTGCTATGGTCCTGGCTGACTTCGGGCGCGGTGTGGTAGCGGTGACCGGCGCCGGCTC	120						
Qy	121	CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGGTAGTGTGGACCTGGAAGCA	180						
Db	121	CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGGTAGTGTGGACCTGGAAGCA	180						
Qy	181	GCCCGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTCCGATGTGCTGTGGAGCC	240						
Db	181	GCCCGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTCCGATGTGCTGTGGAGCC	240						
Qy	241	CTTCCGCGCGGTGTGTCATGGAGAAATCTCAGCTGGGCGCCAGAGATTCTGCAAGCGGAAAA	300						
Db	241	CTTCCGCGCGGTGTGTCATGGAGAAATCTCAGCTGGGCGCCAGAGATTCTGCAAGCGGAAAA	300						
Qy	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGCGTT	360						
Db	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGCGTT	360						
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAG	420						
Db	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAG	420						
Qy	421	TGGTGAAATCCGATGCCCCGCTGAACTCTCTGGCTGACTTTGCTGGTGGTGGCTTAT	480						
Db	421	TGGTGAAATCCGATGCCCCGCTGAACTCTCTGGCTGACTTTGCTGGTGGTGGCTTAT	480						
Qy	481	GTGTGCACTGGGCATTATTAATGGCTCTTTTGGCCGACACGCACTGCAAGGGTCAGGT	540						
Db	481	GTGTGCACTGGGCATTATTAATGGCTCTTTTGGCCGACACGCACTGCAAGGGTCAGGT	540						
Qy	541	CATTGATGCAAAATATGTTGGAGAAACAGCATATTTAAGTCTTTCTGTGGAAACTCA	600						
Db	541	CATTGATGCAAAATATGTTGGAGAAACAGCATATTTAAGTCTTTCTGTGTGGAAACTCA	600						
Qy	601	GAATCCAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGAGACACCTTT	660						
Db	601	GAATCCAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGAGGACACCTTT	660						
Qy	661	CTATACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720						
Db	661	CTATACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720						
Qy	721	GTTCCTACAGCTGCTGATCAAGAGCTTGGACTAAAGTCTGATGAATCCCAATCAGAT	780						
Db	721	GTTCCTACAGCTGCTGATCAAGAGCTTGGACTAAAGTCTGATGAATCTCCCAATCAGAT	780						
Qy	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGTGTTCAGATGTATTTGCAAGAAGAC	840						
Db	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGTGTTCAGATGTATTTGCAAGAAGAC	840						
Qy	841	GAAGGCAGAGTGGTGTCAAACTTTTGAAGGCAAGATGCTGTGACTCCGGTTCTGAC	900						
Db	841	GAAGGCAGAGTGGTGTCAAACTTTTGAAGGCAAGATGCTGTGACTCCGGTTCTGAC	900						
Qy	901	TTTTGAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA	960						
Db	901	TTTTGAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA	960						
Qy	961	GGAGCAGGACGTGAGCCCCCGGCTGCACTCTGCTGTTTAAACACCCAGGCACTCCCTTC	1020						
Db	961	GGAGCAGGACGTGAGCCCCCGGCTGCACTCTGCTGTTTAAACACCCAGGCACTCCCTTC	1020						

Qy	1021	TTTCAAAGGGATCCCTTTTCATAGGAGAACACACACTGAGGAGATACTTTGAAGAAATTTGGATT	1080
Db	1021	TTTCAAAGGGATCCCTTTTCATAGGAGAACACACACTGAGGAGATACTTTGAAGAAATTTGGATT	1080
Qy	1081	CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1140
Db	1081	CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1140
Qy	1141	AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1200
Db	1141	AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1200
Qy	1201	TAGAGTAACACATAACTGTATGTCATGGAACATGCGAGGAACAGTATTTACAGTGTCTTA	1260
Db	1201	TAGAGTAACACATAACTGTATGTCATGGAACATGCGAGGAACAGTATTTACAGTGTCTTA	1260
Qy	1261	CCACTCTAAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGAATGAAATTTCTAAA	1320
Db	1261	CCACTCTAAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGAATGAAATTTCTAAA	1320
Qy	1321	AATGGTTATCATTAGGGCTTTGATTTATAAAATTTGGGTACTTATACATAATATGGT	1380
Db	1321	AATGGTTATCATTAGGGCTTTGATTTATAAAATTTGGGTACTTATACATAATATGGT	1380
Qy	1381	AGTTATTTCTGGCTTCCAGTTTGTGATATATTTGTTGATATTTAAAGATTTCTTGACTTATA	1440
Db	1381	AGTTATTTCTGGCTTCCAGTTTGTGATATATTTGTTGATATTTAAAGATTTCTTGACTTATA	1440
Qy	1441	TTTTGAATGGTCTTCTAGTGAAGAAATGATATATTTCTTGAAGACATCGATATACATTT	1500
Db	1441	TTTTGAATGGTCTTCTAGTGAAGAAATGATATATTTCTTGAAGACATCGATATACATTT	1500
Qy	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGAAATGCCACAAATTTGTATGGTGA	1560
Db	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGAAATGCCACAAATTTGTATGGTGA	1560
Qy	1561	AAAAGTCAGCTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Db	1561	AAAAGTCAGCTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Qy	1621	A 1621	
Db	1621	A 1621	

RESULT 8

US-09-895-814-107
; Sequence 107, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C26
;; CURRENT APPLICATION NUMBER: US/09/895,814
;; CURRENT FILING DATE: 2001-06-29
;; NUMBER OF SEQ ID NOS: 990
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 107
;; LENGTH: 1621
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-895-814-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGACGGGCAATCTCGTCAATGAGCTGTCCGGCTGGCCCGGGCCCGTT 60
DB 1 CGCCATGGCACTGACGGGCAATCTCGTCAATGAGCTGTCCGGCTGGCCCGGGCCCGTT 60

QY 61 CTGTGCTATGCTCTGGCTGACTTCCGGGGCGGTGTGTACGGTGGACCGGGCCGGCTC 120
DB 61 CTGTGCTATGCTCTGGCTGACTTCCGGGGCGGTGTGTACGGTGGACCGGGCCGGCTC 120

QY 121 CGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGTAGTCTGACCTGAAGCA 180
DB 121 CGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGTAGTCTGACCTGAAGCA 180

QY 181 GCCGGGGGAGCGCGCTGCTGGCGCTCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
DB 181 GCCGGGGGAGCGCGCTGCTGGCGCTCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240

QY 241 CTTCCGCGGGGTGTCATGGAGAACTCCAGCTGGGCGGCGAGAGTCTCAGGGGAAAA 300
DB 241 CTTCCGCGGGGTGTCATGGAGAACTCCAGCTGGGCGGCGAGAGTCTCAGGGGAAAA 300

QY 301 TCCAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGGTT 360
DB 301 TCCAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGGTT 360

QY 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTCTCTCAAAAATTGGCAGAAG 420
DB 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTCTCTCAAAAATTGGCAGAAG 420

QY 421 TGGTGAAGATCCGTATGCCCGCGTGAATCTCTGGCTGACTTTGGTGGTGGCTTAT 480
DB 421 TGGTGAAGATCCGTATGCCCGCGTGAATCTCTGGCTGACTTTGGTGGTGGCTTAT 480

QY 481 GTGTGCACTGGGCATTATATGCTCTTTTGGCCGACACGCTGACAGGGTCAGGT 540
DB 481 GTGTGCACTGGGCATTATATGCTCTTTTGGCCGACACGCTGACAGGGTCAGGT 540

QY 541 CATTTGATGCAATATGTTGGAGGAAACAGCATATTTAAGTCTTTCTGTGGAAACTCA 600
DB 541 CATTTGATGCAATATGTTGGAGGAAACAGCATATTTAAGTCTTTCTGTGGAAACTCA 600

QY 601 GAAATCGATCTGTGGGAGGACCTTCAGGACAGAAATGTTGGATGGTGGAGCACTTTT 660
DB 601 GAAATCGATCTGTGGGAGGACCTTCAGGACAGAAATGTTGGATGGTGGAGCACTTTT 660

QY 661 CTATAGCACTTACAGGACAGCATGGGAAATTCATGGCTGTTGGGCAATAGAACCCCA 720
DB 661 CTATAGCACTTACAGGACAGCATGGGAAATTCATGGCTGTTGGGCAATAGAACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTTCCCAATCAGAT 780

QY 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGGAGAC 840
DB 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGGAGAC 840

RESULT 9
US-10-012-896-107
; Sequence 107, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

QY 841 GAAGCGAGAGTGGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900
DB 841 GAAGCGAGAGTGGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900

QY 901 TTTTGGAGGAGTGTTCATCATGATCAAAAGGAAACGGGCTCGTTTATCACCAGTGA 960
DB 901 TTTTGGAGGAGTGTTCATCATGATCAAAAGGAAACGGGCTCGTTTATCACCAGTGA 960

QY 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020
DB 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020

QY 1021 TTTTAAAAGGGATCCTTTTATAGGAGAACACATCAGGAGATATTTGAAGAAATTTGGATT 1080
DB 1021 TTTTAAAAGGGATCCTTTTATAGGAGAACACATCAGGAGATATTTGAAGAAATTTGGATT 1080

QY 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140
DB 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140

QY 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
DB 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200

QY 1201 TAGAGTAACACATAACATTTGATGATGAAACATGAGGAAACAGTATTTACAGTGTCTTA 1260
DB 1201 TAGAGTAACACATAACATTTGATGATGAAACATGAGGAAACAGTATTTACAGTGTCTTA 1260

QY 1261 CCACCTCTAATCAAGAAAGAAATTAAGATCTCTGATTTCTACAGTATGATTTGAATTTCTAAA 1320
DB 1261 CCACCTCTAATCAAGAAAGAAATTAAGATCTCTGATTTCTACAGTATGATTTGAATTTCTAAA 1320

QY 1321 AATGGTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATCTAAATTTATGTT 1380
DB 1321 AATGGTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATCTAAATTTATGTT 1380

QY 1381 AGTTATTTCTGCTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
DB 1381 AGTTATTTCTGCTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440

QY 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
DB 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTCTGATTTCTACATGATGAGAAATGAGAAATGCCAAATTTGATGCTGAT 1560
DB 1501 ATTTACACTCTGATTTCTACATGATGAGAAATGAGAAATGCCAAATTTGATGCTGAT 1560

QY 1561 AAAAGTCACTGAAACAAAAAAGGAAATGAGAAATGCCAAATTTGATGCTGAT 1620
DB 1561 AAAAGTCACTGAAACAAAAAAGGAAATGAGAAATGCCAAATTTGATGCTGAT 1620

QY 1621 A 1621
DB 1621 A 1621

Publication No. US2003008062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42/D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
TYPE: DNA
ORGANISM: Homo sapien
US-10-010-940-107

Query Match 100.0%; Score 1621; DB 6; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCAGTGCAGGCGCATCTCGGTCAATGAGCTGTCCGGCTGGCCCCCGGGCCGGT 60
DB 1 CGCCATGGCAGTGCAGGCGCATCTCGGTCAATGAGCTGTCCGGCTGGCCCCCGGGCCGGT 60

QY 61 CTGTGCTATGTCCTGGCTGACTTGGGGCGGTGTGTGACGCTGGACCGGCCGGCTC 120
DB 61 CTGTGCTATGTCCTGGCTGACTTGGGGCGGTGTGTGACGCTGGACCGGCCGGCTC 120

QY 121 CGCTACGAGCTGAGCGGCTTGGCGGGCGGCAAGCGCTCGTAGTGTGAGCTGAAGCA 180
DB 121 CGCTACGAGCTGAGCGGCTTGGCGGGCGGCAAGCGCTCGTAGTGTGAGCTGAAGCA 180

QY 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
DB 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240

QY 241 CTTCCGCGCGGTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCTCAGCGGGA 300
DB 241 CTTCCGCGCGGTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCTCAGCGGGA 300

QY 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTT 360
DB 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTT 360

QY 361 AGCTGCCAGCATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGA 420
DB 361 AGCTGCCAGCATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGA 420

QY 421 TGGTGAGAAATCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGTGGTGGCTTAT 480
DB 421 TGGTGAGAAATCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGTGGTGGCTTAT 480

QY 481 GTGTGAGCTGGGATTTAATGGCTTTTGGACCGCACAGCATGCAAGGGTCAGT 540
DB 481 GTGTGAGCTGGGATTTAATGGCTTTTGGACCGCACAGCATGCAAGGGTCAGT 540

QY 541 CATTTGATGCAATATCGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAATCTCA 600
DB 541 CATTTGATGCAATATCGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAATCTCA 600

QY 601 GAAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTT 660
DB 601 GAAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTT 660

RESULT 11

US-10-144-678A-107

; Sequence 107, Application US/10144678A

QY 661 CTATACGACTTACAGCAGCAGATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
DB 661 CTATACGACTTACAGCAGCAGATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720

QY 721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780

QY 781 GAGCATGATGATTTGGCCAGAAATCAAGAGAAAGTTTGCAGATGATTTTGAAGAAGAC 840
DB 781 GAGCATGATGATTTGGCCAGAAATCAAGAGAAAGTTTGCAGATGATTTTGAAGAAGAC 840

QY 841 GAAGGACAGTGTGTCCTCAAACTTTGACGGCACAGATGCTGTGTGACTCCCGTTCTGAC 900
DB 841 GAAGGACAGTGTGTCCTCAAACTTTGACGGCACAGATGCTGTGTGACTCCCGTTCTGAC 900

QY 901 TTTTTCAGGAGTGTGTTTCATCATGATCAACAAGGAAAGCGGGCTCGTTTATCACCAGTGA 960
DB 901 TTTTTCAGGAGTGTGTTTCATCATGATCAACAAGGAAAGCGGGCTCGTTTATCACCAGTGA 960

QY 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020
DB 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020

QY 1021 TTTTCAAAAGGATCCTTTTCATAGGAGAAACACACTCAGGAGATACCTTTGAAGAATTTGGATT 1080
DB 1021 TTTTCAAAAGGATCCTTTTCATAGGAGAAACACACTCAGGAGATACCTTTGAAGAATTTGGATT 1080

QY 1081 CAGCGCGGAAGAGATTTTATCAGCTTAACTCAGATATAAATCAATTTGAAGTAAATTAAGTAAA 1140
DB 1081 CAGCGCGGAAGAGATTTTATCAGCTTAACTCAGATATAAATCAATTTGAAGTAAATTAAGTAAA 1140

QY 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
DB 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200

QY 1201 TAGAGTAACACATACTTGTATGATGCAAAACATGGAGGACAGTATTACAGTGTCTTA 1260
DB 1201 TAGAGTAACACATACTTGTATGATGCAAAACATGGAGAACAGTATTACAGTGTCTTA 1260

QY 1261 CCACCTCTAATCAAGAAAAAGAAATTCAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320
DB 1261 CCACCTCTAATCAAGAAAAAGAAATTCAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320

QY 1321 AATGTTATCATTAGGGCTTTTGAATTTATAAACTTTTGGGTACTTTTACTATAATTTATGGT 1380
DB 1321 AATGTTATCATTAGGGCTTTTGAATTTATAAACTTTTGGGTACTTTTACTATAATTTATGGT 1380

QY 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTTAAGATTCTTGACTTATA 1440
DB 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTTAAGATTCTTGACTTATA 1440

QY 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1500
DB 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTTTGATCTCAATGATGAGAAATGAGGAAATGCCAATAATTTGATGGTGTAT 1560
DB 1501 ATTTACACTTTGATCTCAATGATGAGGAAATGAGGAAATGCCAATAATTTGATGGTGTAT 1560

QY 1561 AAAAGTCAGTCAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
DB 1561 AAAAGTCAGTCAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620

QY 1621 A 1621
DB 1621 A 1621

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Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-144-678A-107

Query Match 100.0%; Score 1621; DB 7; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGCGACTGCAGGGGCATCTCGGTCAATGGAGCTGTCGGGCTTGGCCCTGGCCCGGGCCGGT 60
Db 1 CGCCATGCGACTGCAGGGGCATCTCGGTCAATGGAGCTGTCGGGCTTGGCCCTGGCCCGGGCCGGT 60

Qy 61 CTGTGCTATGCTCTCGGCTGACTTCGGGGCGGTGTGTGTACGCTGGACCGCGCCGGCTC 120
Db 61 CTGTGCTATGCTCTCGGCTGACTTCGGGGCGGTGTGTGTACGCTGGACCGCGCCGGCTC 120

Qy 121 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA 180
Db 121 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA 180

Qy 181 GCCCGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGCGATGCTGTGGAGCC 240
Db 181 GCCCGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGCGATGCTGTGGAGCC 240

Qy 241 CTTCCGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCAGAGATTCCTGCAGCGGAAAA 300
Db 241 CTTCCGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCAGAGATTCCTGCAGCGGAAAA 300

Qy 301 TCCAAAGGCTATTATATGCGAGCTCAGTGGATTTCGCCAGTCAGGAAGCTTCTGCGGTT 360
Db 301 TCCAAAGGCTATTATATGCGAGCTCAGTGGATTTCGCCAGTCAGGAAGCTTCTGCGGTT 360

Qy 361 AGCTGGCCAGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAG 420
Db 361 AGCTGGCCAGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAG 420

Qy 421 TGGTCAGAAATCCGATGCCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT 480
Db 421 TGGTCAGAAATCCGATGCCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT 480

Db 421 TGGTGAGAAATCCGATGCCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT 480
Qy 481 GTGTGACATGGGCATTATATATGCTCTTTTGGCCGACACGACCTGACAGGGTCAGGT 540
Db 481 GTGTGACATGGGCATTATATATGCTCTTTTGGCCGACACGACCTGACAGGGTCAGGT 540
Qy 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTCTTTCTGTGGAAAACTCA 600
Db 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTCTTTCTGTGGAAAACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAAGCCTCGAGGACAGAAACATGTTGGATGGTGAGACACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAAGCCTCGAGGACAGAAACATGTTGGATGGTGAGACACCTTT 660
Qy 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
Qy 721 GTTCTAGAGTCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGAT 780
Db 721 GTTCTAGAGTCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAAGATTTGACAGATCTATTTCCAAAGAAAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAAGATTTGACAGATCTATTTCCAAAGAAAGAC 840
Qy 841 GAAGGACAGATGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGATCTCGGTTCTGAC 900
Db 841 GAAGGACAGATGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGATCTCGGTTCTGAC 900
Qy 901 TTTTGGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGGAGGTTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGGACGTGAGCCCCCGCTGCACTCTGCTTAAACACCCCGACCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCCCGCTGCACTCTGCTTAAACACCCCGACCATCCCTTC 1020
Qy 1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGAT 1080
Db 1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGAT 1080
Qy 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACCGGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCCACCGGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAACTTTGTATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Db 1201 TAGAGTAACACATAACTTTGTATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
Qy 1261 CCACCTCTAACTCAAGAAAGAAATTAACAGACTCTGATTTACAGTGTGATTTGAAATTTCTAAA 1320
Db 1261 CCACCTCTAACTCAAGAAAGAAATTAACAGACTCTGATTTACAGTGTGATTTGAAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGAATTTTAAACCTTTGGGTACTTATCTAAATTTATGGT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTTTAAACCTTTGGGTACTTATCTAAATTTATGGT 1380
Qy 1381 AGTTATTTCTGCTTCCAGTTTCTTGTATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTCTTGTATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGTCTTAGTGAAGAAAGGAAATGATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTTAGTGAAGAAAGGAAATGATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTTACACTCTTGTGATCTTACAAATAGAGAAATGAGAAATGCCCAAAATTTGATGGTGAT 1560
Db 1501 ATTTTACACTCTTGTGATCTTACAAATAGAGAAATGAGAAATGCCCAAAATTTGATGGTGAT 1560
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QY 1561 AAAAGTCACGTGAAACAAAAA 1620
Db 1561 AAAAGTCACGTGAAACAAAAA 1620
QY 1621 A 1621
Db 1621 A 1621

RESULT 12
US-10-294-025-107
; Sequence 107, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-107

Query Match 100.0%; Score 1621; DB 7; Length 1621;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCATGGCACTGACGGGCACTCGGTCATGAGCTGTCCGCGCTGGCCCGGCGCGTT 60
Db 1 CGCCATGGCACTGACGGGCACTCGGTCATGAGCTGTCCGCGCTGGCCCGGCGCGTT 60
QY 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTACGGTGGACCGGCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTGTACGGTGGACCGGCGGCTC 120
QY 121 CGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGCTAGTGTCTGACCTGAAGCA 180
Db 121 CGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGCTAGTGTCTGACCTGAAGCA 180
QY 181 GCCGGGGGAGCGCGGCTGCTGGCGGCTGTGTCAAGCGGTGCGATGTCTGCTGGAGCC 240
Db 181 GCCGGGGGAGCGCGGCTGCTGGCGGCTGTGTCAAGCGGTGCGATGTCTGCTGGAGCC 240
QY 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGCGAGGGGAAA 300
Db 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGCGAGGGGAAA 300
QY 301 TCCAGGCTTATTTATGCGAGCTGAGTGATTTGGCCAGTCTGCGGTT 360
Db 301 TCCAGGCTTATTTATGCGAGCTGAGTGATTTGGCCAGTCTGCGGTT 360
QY 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAG 420
Db 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAG 420
QY 421 TGGTGAGAAATCGTATGCCCCGTGAATCTCTGCGTGAATTTGCGGTGGCGCTTAT 480
Db 421 TGGTGAGAAATCGTATGCCCCGTGAATCTCTGCGTGAATTTGCGGTGGCGCTTAT 480
QY 481 GTGTGACCTGGCATTATATGCTCTTTTTCACCGCACGCACTGCAAGGGTCAGGT 540
Db 481 GTGTGACCTGGCATTATATGCTCTTTTTCACCGCACGCACTGCAAGGGTCAGGT 540
QY 541 CATTGATGCAAAATATGGTGGAGGAACAGCATATTTAAGTTCTTTTCTGTGGAACCTCA 600

Db 541 CATTGATGCAAAATATGGTGGAGGAACAGCATATTTAAGTTCTTTTCTGTGGAACCTCA 600
QY 601 GAAATCGAGTCTGTGGAGGACACCTCGAGGACAGAAACATGTTGGATGTTGGAGACCTTT 660
Db 601 GAAATCGAGTCTGTGGAGGACACCTCGAGGACAGAAACATGTTGGATGTTGGAGACCTTT 660
QY 661 CTATACGACTTACAGGACAGCATGTTGGAATTTCAATGCTGTTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCATGTTGGAATTTCAATGCTGTTGGAGCAATAGAACCCCA 720
QY 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT 780
QY 781 GAGCATGATGATGCGCCAGAAATCAAGAAGTGTTCAGATGATTTTGGCAAGAAGAC 840
Db 781 GAGCATGATGATGCGCCAGAAATCAAGAAGTGTTCAGATGATTTTGGCAAGAAGAC 840
QY 841 GAAGCAGAGTGTCTCAAACTTTTGACGGCACAGATGCTGTGACTCCGGTTCGTGAC 900
Db 841 GAAGCAGAGTGTCTCAAACTTTTGACGGCACAGATGCTGTGACTCCGGTTCGTGAC 900
QY 901 TTTTTCAGGAGTGTTCATCATGATCAAAAGGAAACGAGGCTGTTTATCACCAGTGA 960
Db 901 TTTTTCAGGAGTGTTCATCATGATCAAAAGGAAACGAGGCTGTTTATCACCAGTGA 960
QY 961 GGAGCAGGACGTGAGCGCCCGCCCTGACCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCGCCCGCCCTGACCTGCTGTTAAACACCCAGCCATCCCTTC 1020
QY 1021 TTTTCAAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
Db 1021 TTTTCAAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
QY 1081 CAGCGCGGAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTATAAAGTAAA 1140
Db 1081 CAGCGCGGAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTATAAAGTAAA 1140
QY 1141 AGCTAGTCTCTAACTTCCAGGCGCCAGCGCTCAAGTGAATTTGAATCTGCTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCGCCAGCGCTCAAGTGAATTTGAATCTGCTTACAGTG 1200
QY 1201 TAGAGTAACACATAAATTTGATGATGCAATGGAACACATGAGGAAACAGTATTAACAGTGTCTTA 1260
Db 1201 TAGAGTAACACATAAATTTGATGATGCAATGGAACACATGAGGAAACAGTATTAACAGTGTCTTA 1260
QY 1261 CCACCTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
Db 1261 CCACCTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
QY 1321 AATGGTTATCATTAGGGCTTTTGAATTTAATAAATTTGGGTACTTTATTAATTAATTTATGGT 1380
Db 1321 AATGGTTATCATTAGGGCTTTTGAATTTAATAAATTTGGGTACTTTATTAATTAATTTATGGT 1380
QY 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTCATATTAAGATTTCTGACTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTCATATTAAGATTTCTGACTTATA 1440
QY 1441 TTTTGAATGGGTCTTAGTGAAGAAAGGAAATGATATATTTCTTGAAGACATCGATATATTT 1500
Db 1441 TTTTGAATGGGTCTTAGTGAAGAAAGGAAATGATATATTTCTTGAAGACATCGATATATTT 1500
QY 1501 ATTTTACACTCTTGAATTTACAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAAT 1560
Db 1501 ATTTTACACTCTTGAATTTACAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAAT 1560
QY 1561 AAAAGTCACGTGAAACAAAAA 1620
Db 1561 AAAAGTCACGTGAAACAAAAA 1620
QY 1621 A 1621
Db 1621 A 1621

RESULT 13

US-10-688-838-107
; Sequence 107, Application US/10688838
; Publication No. US20040141989A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427D4

; CURRENT APPLICATION NUMBER: US/10/688,838

; CURRENT FILING DATE: 2003-10-17

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-688-838-107

Query Match 100.0%; Score 1621; DB 8; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGCCATGGCACTGACGGGCATCTCGGTCAATGGAGCTGTCGGCCCTGGCCCGCCCGGCGCTT	60
Db	1	CGCCATGGCACTGACGGGCATCTCGGTCAATGGAGCTGTCGGCCCTGGCCCGCCCGGCGCTT	60
Qy	61	CTGTGCTATGTCCTGGCTGATCTCGGGCGGCTGTGTAGCGTGGACCGGCGCGCTC	120
Db	61	CTGTGCTATGTCCTGGCTGATCTCGGGCGGCTGTGTAGCGTGGACCGGCGCGCTC	120
Qy	121	CCGCTACCACTGAGCCGCTTGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	180
Db	121	CCGCTACCACTGAGCCGCTTGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	180
Qy	181	GCCGCGGGAGCGCGCTGTCGGCGCTGTGTCAAGCGGTCGGATGTCGTGGAGCC	240
Db	181	GCCGCGGGAGCGCGCTGTCGGCGCTGTGTCAAGCGGTCGGATGTCGTGGAGCC	240
Qy	241	CTTCGCGCGGCTGTCATGGAGAACTCCAGCTGGCGCCAGAGATTCGCAAGCGGGA	300
Db	241	CTTCGCGCGGCTGTCATGGAGAACTCCAGCTGGCGCCAGAGATTCGCAAGCGGGA	300
Qy	301	TCCAGGCTTATTTATGCCAGGCTCAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360
Db	301	TCCAGGCTTATTTATGCCAGGCTCAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCAAAAAATTGGCAGAG	420
Db	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAAATTGGCAGAG	420
Qy	421	TGTTGAGAAATCGGTATGCCCGCTGAATCTCTCGCTGCACTTGTGTTGGCTTAT	480
Db	421	TGTTGAGAAATCGGTATGCCCGCTGAATCTCTCGCTGCACTTGTGTTGGCTTAT	480
Qy	481	GTGTGCACTGGGCATTTAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGTCAGGT	540
Db	481	GTGTGCACTGGGCATTTAATGGCTCTTTTGGACCGCACAGCACTGACAAAGGTCAGGT	540
Qy	541	CATTGATCAAAATATGGTGGAGGACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCA	600
Db	541	CATTGATCAAAATATGGTGGAGGACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCA	600
Qy	601	GAATTCGAGTCTGTGGAGGACCTCTCGAGGACAGAACTGTGGATGGTGGAGCACTTT	660
Db	601	GAATTCGAGTCTGTGGAGGACCTCTCGAGGACAGAACTGTGGATGGTGGAGCACTTT	660
Qy	661	CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720
Db	661	CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720

RESULT 14

US-11-234-786-107
; Sequence 107, Application US/11234786
; Publication No. US20060024301A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.


```
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-234-786-107

Query Match 100.0%; Score 1621; DB 16; Length 1621;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGGCACTGCGAGGCAATCTCGGTCTATGAGCTGTCCGCCCTGGCCCGGGCCCGGTT 60
Db 1 CGCCATGGCACTGCGAGGCAATCTCGGTCTATGAGCTGTCCGCCCTGGCCCGGGCCCGGTT 60

Qy 61 CTGTGCTATGCTCTGGCTGACTTTCGGGCGGCTGTGCTACGCTGGACCGCCCGGCTC 120
Db 61 CTGTGCTATGCTCTGGCTGACTTTCGGGCGGCTGTGCTACGCTGGACCGCCCGGCTC 120

Qy 121 CGCTACGACGCTGAGCGCTTGGCCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180
Db 121 CGCTACGACGCTGAGCGCTTGGCCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180

Qy 181 GCCGGGGAGCGCGCTGCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGCGAGCC 240
Db 181 GCCGGGGAGCGCGCTGCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGCGAGCC 240

Qy 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCAGAGATTCTGACGGGGA 300
Db 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCAGAGATTCTGACGGGGA 300

Qy 301 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTTCGCCAGTCAGGAAGCTTCTGCCGGTT 360
Db 301 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTTCGCCAGTCAGGAAGCTTCTGCCGGTT 360

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG 420
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG 420

Qy 421 TGGTGAGAAATCCGATATGCCCGCTGAAATCTCTCGCTGACTTTGCTGGTGGTGGCTTAT 480
Db 421 TGGTGAGAAATCCGATATGCCCGCTGAAATCTCTCGCTGACTTTGCTGGTGGTGGCTTAT 480

Qy 481 GTGTGCACTGGGCATTATAATGGCTCTTTTGAACCGCACAGCACTGACAGGGTCAGGT 540
Db 481 GTGTGCACTGGGCATTATAATGGCTCTTTTGAACCGCACAGCACTGACAGGGTCAGGT 540

Qy 541 CATTGATGCAATATGGTGGAGGAGCAAGCATATTAAAGTCTTTTCTGTGGAAGCACTCA 600
Db 541 CATTGATGCAATATGGTGGAGGAGCAAGCATATTAAAGTCTTTTCTGTGGAAGCACTCA 600

Qy 601 GAAATCGAGTCTGTGGGAAAGCACCTCGAGGACAGAAATGTTGGATGCTGGAGCACTTT 660
Db 601 GAAATCGAGTCTGTGGGAAAGCACCTCGAGGACAGAAATGTTGGATGCTGGAGCACTTT 660

Qy 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTGTGAGCAATAGAACCCCA 720

Qy 721 GTTCTACGAGCTGCTGATCAAGGACTTGGAGTAAAGTCTGATGAATTTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGCTGATCAAGGACTTGGAGTAAAGTCTGATGAATTTCCCAATCAGAT 780

Qy 781 GAGCATGATGATTCGCCAGAAAATCAAGAAAGTTCAGATGATTTTGAAGAAAGAC 840
Db 781 GAGCATGATGATTCGCCAGAAAATCAAGAAAGTTCAGATGATTTTGAAGAAAGAC 840

Qy 841 GAAGCAGAGTGGTCTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGAC 900
Db 841 GAAGCAGAGTGGTCTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGAC 900

Qy 901 TTTTGAGAGGTTGTTTCAATCATGATCAACAAGAACGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGAGAGGTTGTTTCAATCATGATCAACAAGAACGGGCTCGTTTATCACCAGTGA 960

Qy 961 GGAGCAGACGCTGAGCCCCCGCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGACGCTGAGCCCCCGCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTC 1020

Qy 1021 TTTCAAAAGGATCCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1080
Db 1021 TTTCAAAAGGATCCCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1080

Qy 1081 CAGCCGCAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAATTAAGGTAAA 1140
Db 1081 CAGCCGCAAGAGATTTATCAGCTTAATCAGATAAAATCAATGAAAGTAAATTAAGGTAAA 1140

Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCTTACAGTGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCTTACAGTGTG 1200

Qy 1201 TAGAGTAACACATAAATTTGATGATGGAACATGAGGAGAACAGTATTAAGTGTCTCTTA 1260
Db 1201 TAGAGTAACACATAAATTTGATGATGGAACATGAGGAGAACAGTATTAAGTGTCTCTTA 1260

Qy 1261 CCATCTTAATCAAGAAAAGATTAAGTGTCTGATTTTACAGTGTGATGATTAAGTGTCTTAA 1320
Db 1261 CCATCTTAATCAAGAAAAGATTAAGTGTCTGATTTTACAGTGTGATGATTAAGTGTCTTAA 1320

Qy 1321 AATGGTATCATAGGGCTTTTGAATTAATAAACTTTGGGTACTTATATAAATATGTT 1380
Db 1321 AATGGTATCATAGGGCTTTTGAATTAATAAACTTTGGGTACTTATATAAATATGTT 1380

Qy 1381 AGTTATTCTGCTTCCAGTTCCTGATATATTTGCTGATATTAAGATTTCTGATCTATA 1440
Db 1381 AGTTATTCTGCTTCCAGTTCCTGATATATTTGCTGATATTAAGATTTCTGATCTATA 1440
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QY 1321 AATGGTTATCATAGGCTTTTGATTTATAAAACCTTTGGTACTTATACCTAAATTTATGGT 1380
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1417 AATGGTTATCATAGGCTTTTGATTTATAAAACCTTTGGTACTTATACCTAAATTTATGGT 1476
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 AGTTATCTGCCTTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1477 AGTTATCTGCCTTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1536
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1441 TTTTGAATGGTTCTAGTGAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1537 TTTTGAATGGTTCTAGTGAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1596
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATCAGGAAATGCCACAAATTTGTATGGTGAT 1560
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1597 ATTTACACTCTTGATTTCTACAATGTAGAAAATCAGGAAATGCCACAAATTTGTATGGTGAT 1656
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1561 AAAAGTCACGTGAACAAA 1579
Db |||||||||||||||
QY 1657 AAAAGTCACGTGAACAGA 1675
Db |||||||||||||||
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Search completed: December 31, 2006, 13:56:06
Job time : 2584.16 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 1259.98 Seconds
(without alignments)
8969.963 Million cell updates/sec

Title: US-09-232-880-107
Perfect score: 1621
Sequence: 1 cccatggcactgcaggcca.....aaaaaaaaaaaaaaaaaaaaa 1621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:
14: geneseqn2005s:
15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1621	100.0	1621	2	AAV58584 Prostate
2	1621	100.0	1621	2	AAV61199 Full leng
3	1621	100.0	1621	3	AAO06347 Human imm
4	1621	100.0	1621	3	ABS71252 Human pro
5	1621	100.0	1621	4	AAH93463 Human pro
6	1621	100.0	1621	4	AAH93463 Human pro
7	1621	100.0	1621	4	AAH02528 Prostate
8	1621	100.0	1621	4	AAH84777 Human pro
9	1621	100.0	1621	5	ACA59364 Prostate
10	1621	100.0	1621	5	AAH10106 Human pro
11	1621	100.0	1621	6	ABL94927 Human Fl-
12	1621	100.0	1621	6	ABS58636 Prostate
13	1621	100.0	1621	8	ACC95091 Prostate
14	1621	100.0	1621	10	ADB13557 Human pro
15	1621	100.0	1621	10	ADG26973 Human pro
16	1621	100.0	1621	15	Aef66254 Human pro
17	1577.4	97.3	2376	5	ABV25239 Human pro
18	1577.4	97.3	2376	5	ABV21293 Human pro

19	1577.4	97.3	2376	5	ABV211881 Human pro
20	1577.4	97.3	2376	5	ABV27112 Human pro
21	1575.8	97.2	1674	4	AaH13696 Human CDN
22	1575.8	97.2	2069	10	ADB75201 Prostate
23	1574.2	97.1	2005	6	AAD38607 Human alp
24	1574.2	97.1	2005	6	AAD38603 Human alp
25	1574.2	97.1	2005	10	ADD18532 Human pro
26	1574.2	97.1	2040	13	ACN38207 Tumour-as
27	1574.2	97.1	2069	6	AAD38604 Human alp
28	1574.2	97.1	2069	10	ADB75193 Prostate
29	1571	96.9	2534	15	AEE20414 Human AWA
30	1524.8	94.1	2068	6	ABK92152 Prostate
31	1524.8	94.1	2068	11	ADN39816 Cancer/an
32	1524.8	94.1	2068	12	ADP56740 Human alp
33	1524.8	94.1	2068	14	ADZ09628 Human bre
34	1245.4	76.8	2946	10	ADB75205 Prostate
35	1245.4	76.8	2946	12	ADP56742 Human alp
36	1243.8	76.7	3023	6	AAD38606 Human alp
37	1243.8	76.7	3023	10	ADB75197 Prostate
38	1134.4	70.0	2626	10	ADB75203 Prostate
39	1132.8	69.9	3654	6	AAD38605 Human alp
40	1132.8	69.9	3654	10	ADB75195 Prostate
41	940	58.0	1039	4	AAC91303 Human pol
42	903.6	55.7	1294	5	ABV22733 Human pro
43	903.6	55.7	1294	5	ABV28442 Human pro
44	903.6	55.7	1294	5	ABV28544 Human pro
45	903.6	55.7	1294	5	ABV22620 Human pro

ALIGNMENTS

RESULT 1
AAV58584
ID AAV58584 standard; cDNA; 1621 BP.
XX AC AAV58584;
XX DT 25-MAR-2003 (revised)
DT 08-DEC-1998 (first entry)
XX DE Prostate tumour specific gene clone Fl-12.
XX KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 5..1153
FT /*tag= a
XX PN WO9837418-A2.
XX PD 27-AUG-1998.
XX PF 25-FEB-1998; 98WO-US003690.
XX PR 25-FEB-1997; 97US-00806596.
PR 01-AUG-1997; 97US-00904809.
PR 09-FEB-1998; 98US-00020747.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC;
XX WPI: 1998-480805/41.
DR P-PSDB; AAW69383.
DR Novel human prostate specific tumour protein and fragments - useful for
PT detecting and treating prostate cancers.
XX Claim 1; Page 81-82; 141pp; English.
PS

xx This sequence represents a human prostate tumour specific gene, and can
cc be used in the method of the invention. The method is for detecting
cc prostate cancer comprises contacting a biological sample with an agent
cc able to bind an immunogenic portion of a prostate protein (such as
cc encoded by this sequence). An antibody which binds to an immunogenic
cc portion of the prostate protein, and the method can be used to detect,
cc monitor progression of, or treat prostate cancers. The antibody may also
cc be conjugated to a therapeutic agent for use in therapy of prostate
cc cancers. (Updated on 25-MAR-2003 to correct PR field.)
xx

SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 2; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGGCACTGCAGGCGCATCTCGTTCATGGAGCTGTCGGCCCTGGCCCGGGCCCGTT 60
Db 1 CGCCATGGCACTGCAGGCGCATCTCGTTCATGGAGCTGTCGGCCCTGGCCCGGGCCCGTT 60

Qy 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGACGCTGGACCGCCCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGACGCTGGACCGCCCGGCTC 120

Qy 121 CGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180
Db 121 CGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180

Qy 181 GCCCGGGAGCGCGCTGTCGCGCTGTGCAAGCGGTGCGATGTCGTGGAGCC 240
Db 181 GCCCGGGAGCGCGCTGTCGCGCTGTGCAAGCGGTGCGATGTCGTGGAGCC 240

Qy 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCCTGCAGCGGAAA 300
Db 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCCTGCAGCGGAAA 300

Qy 301 TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTT 360
Db 301 TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCGCGGTT 360

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAG 420
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAG 420

Qy 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT 480
Db 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTTAT 480

Qy 481 GTGTGCACCTGGCATTATTAAGGCTCTTTTGGACCGCACGCACTGCAAGGTCAGGT 540
Db 481 GTGTGCACCTGGCATTATTAAGGCTCTTTTGGACCGCACGCACTGCAAGGTCAGGT 540

Qy 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600
Db 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600

Qy 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660

Qy 661 CTATACGACTTACAGGACGCGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACGCGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720

Qy 721 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 780

Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGTATTTGCAAGAAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGTATTTGCAAGAAGAC 840

Qy 841 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTTGAC 900
Db 841 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTTGAC 900

Qy 901 TTTTGGAGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCACTGA 960
Db 901 TTTTGGAGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCACTGA 960

Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTGTTAAACACCCAGCCATCCCTTC 1020

Qy 1021 TTTTCAAAAGGATCTCTTTTCATAGAGAAACACACTGAGGAGATACTTGAAGAAATTTGATT 1080
Db 1021 TTTTCAAAAGGATCTCTTTTCATAGAGAAACACACTGAGGAGATACTTGAAGAAATTTGATT 1080

Qy 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140

Qy 1141 AGTAGTCTCTAACTCCAGGCCCA CGGCTCAAGTGAATTTGAATACCTGCAATTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTCCAGGCCCA CGGCTCAAGTGAATTTGAATACCTGCAATTACAGTG 1200

Qy 1201 TAGAGTAAACATAAATCTGTATGTCATGGAAACATGAGGAAACAGATATTACAGTGTCTA 1260
Db 1201 TAGAGTAAACATAAATCTGTATGTCATGGAAACATGAGGAAACAGATATTACAGTGTCTA 1260

Qy 1261 CCACCTTAATCAAGAAAGAAATTAACAGACTCTGATCTTACAGTGATGATTAATTTCTAAA 1320
Db 1261 CCACCTTAATCAAGAAAGAAATTAACAGACTCTGATCTTACAGTGATGATTAATTTCTAAA 1320

Qy 1321 AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATTAATAATATGGT 1380
Db 1321 AATGGTTATCATTTAGGCTTTTGAATTTATAAACTTTGGGTACTTATTAATAATATGGT 1380

Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTAAGATTTCTTGACTTATA 1440

Qy 1441 TTTTGAATGGTTCCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTTCCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500

Qy 1501 ATTTACACTCTGATTTCTACATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTGAT 1560
Db 1501 ATTTACACTCTGATTTCTACATGTAGAAAATGAGGAAATGCCACAAATTTGATGGTGAT 1560

Qy 1561 AAAAGTCACGTGAACAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1620
Db 1561 AAAAGTCACGTGAACAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1620

Qy 1621 A 1621
Db 1621 A 1621

RESULT 2
AAV61199
ID AAV61199 standard; cDNA; 1621 BP.
XX
AC AAV61199;
XX
DT 06-JAN-1999 (first entry)
XX
Full length cDNA sequence of prostate tumour clone FI-12.
XX
Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
Homo sapiens.
XX
PN W09837093-A2.
XX

PD	27-AUG-1998.
XX	
XX	25-FEB-1998; 98WO-US003492.
PF	
XX	
XX	25-FEB-1997; 97US-00806099.
PR	01-AUG-1997; 97US-00904804.
PR	09-FEB-1998; 98US-00020956.
XX	
XX	(CORI-) CORIXA CORP.
PA	
XX	Xu J, Dillon DC;
PI	
XX	WPI; 1998-609886/51.
DR	P-PSDB; AAW71867.
XX	
PT	Polypeptides comprising immunogenic portions of prostate proteins - used
PT	in a vaccine for the treatment of prostate cancer.
XX	
PS	Claim 3; Page 76-77; 130pp; English.
XX	
CC	The present sequence is a new DNA which encodes an immunogenic portion of
CC	a prostate tumour protein. The encoded immunogen, or the DNA itself, can
CC	be used as a vaccine for the treatment of prostate cancer. The DNA was
CC	identified by analysis of a subtracted cDNA library obtained by
CC	subtracting a prostate tumour cDNA expression library with a normal
CC	tissue cDNA library
XX	
SQ	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1621; DB 2; Length 1621;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGCCATGCACTGCAGGGCATCTCGGTCAANGAGCTTCFCGGCCTGCCCCGGGCCCGTTT 60
Db	1 CGCCATGCACTGCAGGGCATCTCGGTCAATGAGCTTCFCGGCCTGCCCCGGGCCCGTTT 60
QY	61 CTGTGCTATTGTCCTGGCTGACTTCGGGGCGCGTGCTACGGCTGACCGGCCGGCTC 120
Db	61 CTGTGCTATTGTCCTGGCTGACTTCGGGGCGCGTGCTACGGCTGACCGGCCGGCTC 120
QY	121 CGCGTACGACGTAGCCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
Db	121 CGCGTACGAGTGTAGCCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
QY	181 GCCCGGGGAGCCGCGTGTGTCGGCGCTGTGTGCAAGCGTFCGATGTGCTGTGAGCC 240
Db	181 GCCCGGGGAGCCGCGTGTGTCGGCGCTGTGTGCAAGCGTFCGATGTGCTGTGAGCC 240
QY	241 CTTTCGCGCGGTGTTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAAA 300
Db	241 CTTTCGCGCGGTGTTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAAA 300
QY	301 TCACAAGGCTTAATTTATGCGAGGCTGAGTGGATTGGCCAGTAGCAGGAAGCTTCTGCCGGTT 360
Db	301 TCACAAGGCTTAATTTATGCGAGGCTGAGTGGATTGGCCAGTAGCAGGAAGCTTCTGCCGGTT 360
QY	361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAG 420
Db	361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAG 420
QY	421 TGGTCAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGGCTTAT 480
Db	421 TGGTCAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGGCTTAT 480
QY	481 GTGTGCACCTGGGCAATTATAATGGCTCTTTTTTGACCGCACACGCACTGACAAGGGTCAGGT 540
Db	481 GTGTGCACCTGGGCAATTATAATGGCTCTTTTTTGACCGCACACGCACTGACAAGGGTCAGGT 540
QY	541 CATTCATGCAAAATATGTTGGAAGGAAACAGCANATTTAAAGTTCCTTTCTGTGAAAACTCA 600
Db	541 CATTCATGCAAAATATGTTGGAAGGAAACAGCANATTTAAAGTTCCTTTCTGTGAAAACTCA 600

Db 1261 CCACCTCAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGATGATGAATTTCTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGGATTATATAAACTTTGGTACTTATATCTAAATATGTT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGGATTATATAAACTTTGGTACTTATATCTAAATATGTT 1380
Qy 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTTGTGATATTTTGTGATTTTAAAGATTCTTGACTTATA 1440
Db 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTTGTGATATTTTGTGATTTTAAAGATTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCATGATATACATTT 1500
Db 1441 TTTTGAATGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCATGATATACATTT 1500
Qy 1501 ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGTGAT 1560
Db 1501 ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGTGAT 1560
Qy 1561 AAAAGTCACGTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1620
Db 1561 AAAAGTCACGTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 4
ABS71252
ID ABS71252 standard; cDNA; 1621 BP.
XX AC ABS71252;
XX DT 27-NOV-2002 (first entry) *
XX DE Human prostate tumour protein partial gene sequence #1.
XX KW Human; immunogenic; prostate protein; prostate tumour protein;
XX KW prostate cancer; cytostatic; vaccine; gene; ss.
XX OS Homo sapiens.
XX PN US2002090372-A1.
XX PD 11-JUL-2002.
XX PF 14-JUL-1998; 98US-00115453.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 09-FEB-1998; 98US-00020956.
XX PR 25-FEB-1998; 98US-00030607.
XX (XUJJ/) XU J.
XX PA (DILL/) DILLON D C.
XX PI Xu J, Dillon DC;
XX DR WPI; 2000-171268/15.
XX DR P-PSDB; ABG94409.
XX PT New polypeptide useful for treating and diagnosing prostate cancer
XX PT comprises an immunogenic portion of prostate tumor protein.
XX PS Claim 3; Page 54; 101pp; English.
XX CC The present invention relates to a new polypeptide comprising an
XX CC immunogenic portion of a prostate protein. The invention is useful for
XX CC inhibiting the development of prostate cancer in a patient. The invention
XX CC is also useful as markers for diagnosing prostate cancer and for
XX CC monitoring diseases progression in patients. The present nucleic acid
XX CC sequence represents a DNA sequence that is part of a gene encoding a
XX CC human prostate tumour protein

XX SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCCATGACACTGACAGGCACTCTCGGTTCATGAGCTGTCCGGCTTGGCCCGGGCCCGCTT 60
Db 1 GCCCATGACACTGACAGGCACTCTCGGTTCATGAGCTGTCCGGCTTGGCCCGGGCCCGCTT 60
Qy 61 CTGTGCTATGTCCTGGCTGACTTCCGGGCGCGTGTGTACCGGTGAGCCCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCCGGGCGCGTGTGTACCGGTGAGCCCGGCTC 120
Qy 121 CGCTTACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 180
Db 121 CGCTTACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 180
Qy 181 GCCGCGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGCGAGCC 240
Db 181 GCCGCGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGCGAGCC 240
Qy 241 CTTCCGCGCGGTGTCTATGAGAACTCCAGCTGGGCGGAGAGATTTGCGAGCGGAAAA 300
Db 241 CTTCCGCGCGGTGTCTATGAGAACTCCAGCTGGGCGGAGAGATTTGCGAGCGGAAAA 300
Qy 301 TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCGGCTTCTCAAAAAATGGCAGAG 360
Db 301 TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCGGCTTCTCAAAAAATGGCAGAG 360
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATGGCAGAG 420
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATGGCAGAG 420
Qy 421 TGGTGAGAAATCGTATGCCCGCTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 480
Db 421 TGGTGAGAAATCGTATGCCCGCTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTTAT 480
Qy 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 CATTTGATGCAAAATATGTTGGAAGAAACAGCATATTTAAAGTCTTTCTGTGAAAACTCA 600
Db 541 CATTTGATGCAAAATATGTTGGAAGAAACAGCATATTTAAAGTCTTTCTGTGAAAACTCA 600
Qy 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT 660
Db 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGAGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780
Qy 781 GAGCATGATGATGGCCAGAAATGAAGAAAGTTTCAGATGATTTTGGAAAAAGAAC 840
Db 781 GAGCATGATGATGGCCAGAAATGAAGAAAGTTTCAGATGATTTTGGAAAAAGAAC 840
Qy 841 GAGGCAGATGGTGTCAAACTTTGACGGCAGATGCTGTGACTCTCGGTTCTGAC 900
Db 841 GAGGCAGATGGTGTCAAACTTTGACGGCAGATGCTGTGACTCTCGGTTCTGAC 900
Qy 901 TTTTTCAGAGGTTGTTTCAATCATGATCAACAAAGGAAACGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTTCAGAGGTTGTTTCAATCATGATCAACAAAGGAAACGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGGACGTGAGCCCGGCTGACCTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCGGCTGACCTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020

Db 961 GGAGCAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCGCCATCCCTTC 1020
Qy 1021 TTTCAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATATCTTGAAGAAATTTGGATT 1080
Db 1021 TTTCAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATATCTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCCGCAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAATAGGTAAA 1140
Db 1081 CAGCCGCAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAATAGGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTTGAATCTACTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTTGAATCTACTGCAATTTACAGTG 1200
Qy 1201 TAGAGTACACATAACATTTGATGATCGATGGAACATGAGGAGACAGTATTACAGTGTCTTA 1260
Db 1201 TAGAGTACACATAACATTTGATGATCGATGGAACATGAGGAGACAGTATTACAGTGTCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTACAGTGAATTTGAATTTCTAAA 1320
Db 1261 CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTACAGTGAATTTGAATTTCTAAA 1320
Qy 1321 AATGGTTATCATAGGGCTTTTGATTTATAAACTTTGGGTACTTATATAAAATTTATGGT 1380
Db 1321 AATGGTTATCATAGGGCTTTTGATTTATAAACTTTGGGTACTTATATAAAATTTATGGT 1380
Qy 1381 AGTTATCTGCTTCCAGTTTCTTGATATATTTTGTGATATTAAGATTTCTGACTTATA 1440
Db 1381 AGTTATCTGCTTCCAGTTTCTTGATATATTTTGTGATATTAAGATTTCTGACTTATA 1440
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTCTATGGTGAT 1560
Db 1501 ATTTACACTCTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTCTATGGTGAT 1560
Qy 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Db 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 5

AAH93463
ID AAH93463 standard; cDNA; 1621 BP.

XX AC AAH93463;

XX DT 04-OCT-2001 (first entry)

XX DE Human prostate-specific full length cDNA sequence F1-12.

XX DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200151633-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001574.

XX PR 14-JAN-2000; 2000US-00483672.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX Claim 1; Page 262-263; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 4; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATGCGCATCTGCGGCGCTTCGCTCATGAGAGTCTCGGCGCTGCGCCCGCGCGCTT 60

Db 1 CGCATGCGCATCTGCGGCGCTTCGCTCATGAGAGTCTCGGCGCTGCGCCCGCGCGCTT 60

Qy 61 CTGTGCTATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 61 CTGTGCTATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy 121 CCGCTACGACGTGAGCGCGCTTGGCGCCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180

Db 121 CCGCTACGACGTGAGCGCGCTTGGCGCCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180

Qy 181 GCGCGGGGAGCGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240

Db 181 GCGCGGGGAGCGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240

Qy 241 CTTCCCGCGCGGCTCTCATGAGAACTCCAGCTGGGCGCCAGAGATTTCTGAGCGGGGAAAA 300

Db 241 CTTCCCGCGCGGCTCTCATGAGAACTCCAGCTGGGCGCCAGAGATTTCTGAGCGGGGAAAA 300

Qy 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCTGCCGGTT 360

Db 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCTGCCGGTT 360

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTTGTCAAGGTGTTCTCTCAAAAATTTGCGAGAAG 420

Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTTGTCAAGGTGTTCTCTCAAAAATTTGCGAGAAG 420

Qy 421 TGGTGAGAAATCCGTATGCGCGCGCTGGAATCTCCGCTGAGCTTTGCTGGTGGCTTTAT 480

Db 421 TGGTGAGAAATCCGTATGCGCGCGCTGGAATCTCCGCTGAGCTTTGCTGGTGGCTTTAT 480

Qy 481 GTGTGCACCTGGGCAATTATAATGGCTCTTTTGTGACCGCACGCACTGACAGGCTCAGGT 540

Db 481 GTGTGCACCTGGGCAATTATAATGGCTCTTTTGTGACCGCACGCACTGACAGGCTCAGGT 540

Qy 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 600

Db 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 600

Qy 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGTTGGGACACCTTT 660

Db 601 GAAATCGAGTCTGTGGAGCACCTCGAGGACAGAACTGTTGGATGGTGAGCACCTTT 660
Qy 661 CTATACGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTCTGATCAAGGACTTTGAGCTAAAGTCTGATGAATCTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTCTGATCAAGGACTTTGAGCTAAAGTCTGATGAATCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 840
Qy 841 GAAGGCAGAGTGTGTCTTTCAGCGCACAGATGCTGTGCTCACTCCGGTCTTGAC 900
Db 841 GAAGGCAGAGTGTGTCTTTCAGCGCACAGATGCTGTGCTCACTCCGGTCTTGAC 900
Qy 901 TTTTGAAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCACTGA 960
Db 901 TTTTGAAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCACTGA 960
Qy 961 GGAGCAGGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTTCAAAAGGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGAT 1080
Db 1021 TTTTCAAAAGGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGAT 1080
Qy 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGTAAA 1140
Db 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGTAAA 1140
Qy 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAACATTTGATGATGAAACATCGAGGAGACAGTATTACAGTGCTTA 1260
Db 1201 TAGAGTAACACATAACATTTGATGATGAAACATCGAGGAGACAGTATTACAGTGCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGATGATTAATCTTAA 1320
Db 1261 CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGATGATTAATCTTAA 1320
Qy 1321 AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATCTAAATTTATGTT 1380
Db 1321 AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATCTAAATTTATGTT 1380
Qy 1381 AGTTATCTGCTTCAGTTTGTGTTGATATATTTGTTGATATTAAGATCTTGAATTTATA 1440
Db 1381 AGTTATCTGCTTCAGTTTGTGTTGATATATTTGTTGATATTAAGATCTTGAATTTATA 1440
Qy 1441 TTTTGAATGGTCTAGTGAAGAAAGCAATATATTTCTGAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTAGTGAAGAAAGCAATATATTTCTGAGACATCGATATACATTT 1500
Qy 1501 ATTTTACACTCTTGATTTCTACAAATGTAGAAATGAGGAAATGCCACAAATTTGATGGTAT 1560
Db 1501 ATTTTACACTCTTGATTTCTACAAATGTAGAAATGAGGAAATGCCACAAATTTGATGGTAT 1560
Qy 1561 AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1620
Db 1561 AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 6

AAS63555
ID AAS63555 standard; cDNA; 1621 BP.
AC AAS63555;
XX 29-JAN-2002 (first entry)
XX Human prostate cDNA sequence #107.
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX WO200173032-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US009919.
XX 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI: 2001-639232/73.
DR P-PSDB; AAU69761.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS Claim 1; Page 264-265; 579pp; English.
XX
CC The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 100.0%; Score 1621; DB 4; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCCATGGCACTGACGGGCATCTCGGTTCATGGAGTGTCCGGCTGGCCCGGCGCGTT 60
Db 1 CGCCATGGCACTGACGGGCATCTCGGTTCATGGAGTGTCCGGCTGGCCCGGCGCGTT 60
Qy 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGTACGCTGGACCGGCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGTACGCTGGACCGGCGGCTC 120
Qy 121 CCGCTACGACGTGAGCCGCTTGGGCGGCAAGCGCTCGCTAGTGTGCTGAGCACTGAAGCA 180

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Db 121 |CGCTACACGTGAGCCCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA 180
Qy 181 |GCCGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTCGATGCTGCTGGAGCC 240
Db 181 |GCCGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTCGATGCTGCTGGAGCC 240
Qy 241 |CTTCGCGCGGGTGCATGAGAAATCTCAGCTGGGCCCAGAGATTCGTGACGGGAAAA 300
Db 241 |CTTCGCGCGGGTGCATGAGAAATCTCAGCTGGGCCCAGAGATTCGTGACGGGAAAA 300
Qy 301 |TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGTT 360
Db 301 |TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGTT 360
Qy 361 |AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATGGCAGAG 420
Db 361 |AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATGGCAGAG 420
Qy 421 |TGGTGAGAAATCGTATGCCCCGCTGAATCTCTGCTGGCTGACTTTGCTGGTGGCTTAT 480
Db 421 |TGGTGAGAAATCGTATGCCCCGCTGAATCTCTGCTGGCTGACTTTGCTGGTGGCTTAT 480
Qy 481 |GTGTGCACTGGGCACTTATAATGGCTCTTTTGGACCGCACGCACTGCAAGGGTTCAGGT 540
Db 481 |GTGTGCACTGGGCACTTATAATGGCTCTTTTGGACCGCACGCACTGCAAGGGTTCAGGT 540
Qy 541 |CATTTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCA 600
Db 541 |CATTTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCA 600
Qy 601 |GAAATCGAGTCTGTGGGAGGACCTCGAGGACAGAAACATGTTGGATGTTGAGGACACCTTT 660
Db 601 |GAAATCGAGTCTGTGGGAGGACCTCGAGGACAGAAACATGTTGGATGTTGAGGACACCTTT 660
Qy 661 |CTATACGACTTACAGGACAGCATGCGGAATTCATGCTGTTGGAGCAATAGAACCCCA 720
Db 661 |CTATACGACTTACAGGACAGCATGCGGAATTCATGCTGTTGGAGCAATAGAACCCCA 720
Qy 721 |GTTCTACGAGTCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Db 721 |GTTCTACGAGTCTGTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGAT 780
Qy 781 |GAGCATGATGATGCGGAGAAATGAAGAAGTTTGCAGATGATTTGCAAGAAGAC 840
Db 781 |GAGCATGATGATGCGGAGAAATGAAGAAGTTTGCAGATGATTTGCAAGAAGAC 840
Qy 841 |GAAGGACAGTGGTGTCAAACTCTTTGACGGCACAGATGCTGTGAGCTCCGGTTCTGAC 900
Db 841 |GAAGGACAGTGGTGTCAAACTCTTTGACGGCACAGATGCTGTGAGCTCCGGTTCTGAC 900
Qy 901 |TTTTGAGGAGTGTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960
Db 901 |TTTTGAGGAGTGTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960
Qy 961 |GGAGCAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020
Db 961 |GGAGCAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020
Qy 1021 |TTTCAAAAGGGATCTTTTCATAGGAGAACACACTCAGGAGATCTTGAAGATTTGGATT 1080
Db 1021 |TTTCAAAAGGGATCTTTTCATAGGAGAACACACTCAGGAGATCTTGAAGATTTGGATT 1080
Qy 1081 |CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAA 1140
Db 1081 |CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAA 1140
Qy 1141 |AGCTAGTCTCTAACTTCCAGGCCACCGGCTCAAGTGAATTTGAATFACATGCAATTACAGTG 1200
Db 1141 |AGCTAGTCTCTAACTTCCAGGCCACCGGCTCAAGTGAATTTGAATFACATGCAATTACAGTG 1200
Qy 1201 |TAGAGTAACATAACATGTTATGATGGAACATGGGAGACATATTACAGTCTCCTA 1260
Db 1201 |TAGAGTAACATAACATGTTATGATGGAACATGGGAGACATATTACAGTCTCCTA 1260
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Db 1201 |TAGAGTAACATAACATGTTGATGTCATGGAAAACATGGAGGAAACAGTATTACAGTGTCTTA 1260
Qy 1261 |CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1320
Db 1261 |CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1320
Qy 1321 |AATGGTTATCATTTAGGCTTTTGTATTTATATAAACTTTGGGTACTTATACATAAATATGGT 1380
Db 1321 |AATGGTTATCATTTAGGCTTTTGTATTTATATAAACTTTGGGTACTTATACATAAATATGGT 1380
Qy 1381 |AGTTATTTCTGCTTCCAGTTTGTCTGATATATTTTGTGATATTAAAGATTTCTTGACTTATA 1440
Db 1381 |AGTTATTTCTGCTTCCAGTTTGTCTGATATATTTTGTGATATTAAAGATTTCTTGACTTATA 1440
Qy 1441 |TTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 |TTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 |ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCCAAAATTTGTATGGTGAT 1560
Db 1501 |ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCCAAAATTTGTATGGTGAT 1560
Qy 1561 |AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
Db 1561 |AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
Qy 1621 |A 1621
Db 1621 |A 1621
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RESULT 7

AAH02528
ID AAH02528 standard; cDNA; 1621 BP.

XX AC AAH02528;

XX AC
DT 14-JUN-2001 (first entry)

XX Prostate tumour antigen determined full length cDNA sequence for Fl-12.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
XX prostate cancer; immunogenic; cytostatic; vaccine; ss.

XX Homo sapiens.

XX WO200125272-A2.

XX PD 12-APR-2001.

XX PF 04-OCT-2000; 2000WO-US027464.

XX PR 04-OCT-1999; 99US-0157455P.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Skeiky YAW, Reed SG, Cheever MA;

XX DR WPI; 2001-245062/25.

XX DR P-PSDB; AAB74798.

XX Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.

XX Claim 4; Page 153; 276pp; English.

XX The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate

CC specific proteins and oligonucleotides that hybridise to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AA02422 to AA2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 4; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGCGATCTCGGTCAATGAGCTGTCCGGCTCGGCCCGCCGGCCCGGT 60
DB 1 CGCCATGGCACTGCAGGCGATCTCGGTCAATGAGCTGTCCGGCTCGGCCCGCCGGCCCGGT 60
QY 61 CTGTGCTATGGTCTCGCTGACTTCGGGCGCGTGTGTACGCGTGGACCGGCCCGCTC 120
DB 61 CTGTGCTATGGTCTCGCTGACTTCGGGCGCGTGTGTACGCGTGGACCGGCCCGCTC 120
QY 121 CGCTACGAGCTGAGCGGCTTGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180
DB 121 CGCTACGAGCTGAGCGGCTTGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180
QY 181 GCGCGGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
DB 181 GCGCGGGGAGCGCGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240
QY 241 CTTCCGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGACGGGAAA 300
DB 241 CTTCCGCGCGGTGTCAATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGACGGGAAA 300
QY 301 TCAAGGCTTATTTATGCAAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTT 360
DB 301 TCAAGGCTTATTTATGCAAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCGGTT 360
QY 361 AGTGTCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAG 420
DB 361 AGTGTCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAG 420
QY 421 TGGTGAGATCCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTAT 480
DB 421 TGGTGAGATCCGTATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTAT 480
QY 481 GTGTGCACTGGGCAATTAATGGCTCTTTTGGCCGACACGCACTGCAAGGTCAGGT 540
DB 481 GTGTGCACTGGGCAATTAATGGCTCTTTTGGCCGACACGCACTGCAAGGTCAGGT 540
QY 541 CATTTGATGCAATATGTTGGAGGACAGCATATTTAAGTCTTTTCTGTTGGAAGTCA 600
DB 541 CATTTGATGCAATATGTTGGAGGACAGCATATTTAAGTCTTTTCTGTTGGAAGTCA 600
QY 601 GAAATCGAGTCTGTGGAGAGCCTCGAGGACAGAACTGTTGGATGTTGGAGCACTTTT 660
DB 601 GAAATCGAGTCTGTGGAGAGCCTCGAGGACAGAACTGTTGGATGTTGGAGCACTTTT 660
QY 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATGAACCCCA 720
DB 661 CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATGAACCCCA 720
QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGATTAAGTCTGATGACTTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGGATTAAGTCTGATGACTTCCCAATCAGAT 780
QY 781 GAGCATGAGTATGTTGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAGAC 840
DB 781 GAGCATGAGTATGTTGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAGAC 840
QY 841 GAAGGCAGAGTGGTGTCAAACTTTTGAACGCGACAGATGCTGTGTGACTCCGGTTCTGAC 900
DB 841 GAAGGCAGAGTGGTGTCAAACTTTTGAACGCGACAGATGCTGTGTGACTCCGGTTCTGAC 900

QY 901 TTTTGGAGGAGTGTTCATCATGATCAACAAGAAACGGGCTCGTTTATCACCAGTGA 960
DB 901 TTTTGGAGGAGTGTTCATCATGATCAACAAGAAACGGGCTCGTTTATCACCAGTGA 960
QY 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCCGACCATCCCTTC 1020
DB 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCCGACCATCCCTTC 1020
QY 1021 TTTTAAAAAGGATCCTTTTCATAGGAGAAACACACTCAGAGATACATTGAAGAAATTTGGATT 1080
DB 1021 TTTTAAAAAGGATCCTTTTCATAGGAGAAACACACTCAGAGATACATTGAAGAAATTTGGATT 1080
QY 1081 CAGCCCGCAAGAGATTATCAGCTTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1140
DB 1081 CAGCCCGCAAGAGATTATCAGCTTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1140
QY 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATACATGCTTACAGTG 1200
DB 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATACATGCTTACAGTG 1200
QY 1201 TAGAGTAACACATAACATTTGTATGATGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
DB 1201 TAGAGTAACACATAACATTTGTATGATGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260
QY 1261 CCACCTCTAATCAAGAAAAAGATTACAGACTCTGATTCTACAGTGTGATTTGAATTTCTAAA 1320
DB 1261 CCACCTCTAATCAAGAAAAAGATTACAGACTCTGATTCTACAGTGTGATTTGAATTTCTAAA 1320
QY 1321 AATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATAATTTATGTT 1380
DB 1321 AATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATAATTTATGTT 1380
QY 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440
DB 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440
QY 1441 TTTTCAATGGGTTCTAGTGAAAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1500
DB 1441 TTTTCAATGGGTTCTAGTGAAAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1500
QY 1501 ATTTACACTCTTGTATCTCAATGATGAAAAATGAGGAAATGCCAAATTTGATGTTGAT 1560
DB 1501 ATTTACACTCTTGTATCTCAATGATGAAAAATGAGGAAATGCCAAATTTGATGTTGAT 1560
QY 1561 AAAAGTCACTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
DB 1561 AAAAGTCACTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
QY 1621 A 1621
DB 1621 A 1621
RESULT 8
AAH84777
ID AAH84777 standard; cDNA; 1621 BP.
XX
AC AAH84777;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence F1-12/P504S.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX

PF	09-NOV-2000; 2000MO-US030904.	QY	541	CATTGATGCAATATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTTCTGTGGAAAACTCA	600
XX		Db	541	CATTGATGCAATATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTTCTGTGGAAAACTCA	600
PR	12-NOV-1999; 99US-00439313.	QY	601	GAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATCTTGGATGGTGGAGCACCTTT	660
PR	18-NOV-1999; 99US-00443686.	Db	601	GAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATCTTGGATGGTGGAGCACCTTT	660
XX	(CORI-) CORIXA CORP.				
XX					
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;	QY	661	CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;	Db	661	CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720
XX	WPI; 2001-308785/32.				
XX					
PT	Isolated polypeptide comprising at least an immunogenic portion of a	QY	721	GTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT	780
PT	prostate-specific protein, useful in the diagnosis and therapy of	Db	721	GTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT	780
XX	prostate cancer.				
XX					
PS	Claim 5; Page 162-163; 325pp; English.	QY	781	GAGCATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCCAAAGAAGAC	840
PS		Db	781	GAGCATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCCAAAGAAGAC	840
CC	The present invention describes an isolated polypeptide (P1) comprising	QY	841	GAAGCGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCGGTCTTGAC	900
CC	at least an immunogenic portion of a prostate-specific protein, or its	Db	841	GAAGCGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCGGTCTTGAC	900
CC	variant. Also described are polynucleotides (N1) encoding (P1). (P1) and				
CC	(N1) have cytotstatic activity and can be used in vaccine production. The				
CC	polypeptides, nucleic acids and antibodies from the present invention are				
CC	useful in the diagnosis and therapy of prostate cancer. Prostate specific				
CC	genes P704P, P712P, P774P, P775P and B305D are located in a genomic	QY	901	TTTTGAGAGGTTGTTTCATCATGATCACAACAGGAACGGGCTCGTTTATCACCAGTGA	960
CC	region on chromosome 22q11.2 known as the Cat Eye Syndrome region.	Db	901	TTTTGAGAGGTTGTTTCATCATGATCACAACAGGAACGGGCTCGTTTATCACCAGTGA	960
CC	Prostate specific antigen (PSA) P501S was located on chromosome 1.	QY	961	GGAGCAGGACGTGAGCCCCCGCTGCACTCTGCTGTAAACACCCAGCCATCCCTTC	1020
CC	AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide	Db	961	GGAGCAGGACGTGAGCCCCCGCTGCACTCTGCTGTAAACACCCAGCCATCCCTTC	1020
CC	and polypeptide sequences used in the exemplification of the present				
CC	invention				
XX					
SQ	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;				
	Query Match 100.0%; Score 1621; DB 4; Length 1621;				
	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 CGCCATGACACTGAGGGCATCTCGTCAATGAGCTGTCGGGCTGGCCCCCGGGCCCGTT	60			
Db	1 CGCCATGACACTGAGGGCATCTCGTCAATGAGCTGTCGGGCTGGCCCCCGGGCCCGTT	60			
QY	61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTGTGCTGAGCGGCGGCGGCTC	120			
Db	61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTGTGCTGAGCGGCGGCGGCTC	120			
QY	121 CCGCTACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCA	180			
Db	121 CCGCTACGACGTGAGCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCA	180			
QY	181 GCCGGGGAGCGCGCTGTGCGGCGTCTGTGAAGCGGTCCGATGTGCTGGAGCC	240			
Db	181 GCCGGGGAGCGCGCTGTGCGGCGTCTGTGAAGCGGTCCGATGTGCTGGAGCC	240			
QY	241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCGGCGAGATTCGACAGCGGAAAA	300			
Db	241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCGGCGAGATTCGACAGCGGAAAA	300			
QY	301 TCCAGGCTTATTTATGCGAGGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTGCGGTT	360			
Db	301 TCCAGGCTTATTTATGCGAGGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTGCGGTT	360			
QY	361 AGCTGGCCACAGATCAACTATTTGGCTTTGTGAGGTTGTCCTCAAAAAATGGCAGAG	420			
Db	361 AGCTGGCCACAGATCAACTATTTGGCTTTGTGAGGTTGTCCTCAAAAAATGGCAGAG	420			
QY	421 TGGTGAGAAATCCGTAATGCGGCTGAATCTCTGAGGTTGTTCTCAAAAAATGGCAGAG	480			
Db	421 TGGTGAGAAATCCGTAATGCGGCTGAATCTCTGAGGTTGTTCTCAAAAAATGGCAGAG	480			
QY	481 GTGTGACTGGGCATTTAATGGCTCTTTTGAACCGCACACGCACTGACAGGGGTCAAGT	540			
Db	481 GTGTGACTGGGCATTTAATGGCTCTTTTGAACCGCACACGCACTGACAGGGGTCAAGT	540			

CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1621;	DB 5;	Length 1621;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1621;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGCCATGCGACCTGCGAGGCGATCTCGGTCTATGAGCTGTCCGGCTCGCCCGCCGCGCTT	60	
DB	1	CGCCATGCGACCTGCGAGGCGATCTCGGTCTATGAGCTGTCCGGCTCGCCCGCCGCGCTT	60	
QY	61	CTGTGCTATGGTCTCTGGCTGACTTTCGGGCGCGGTGTGGTACGCGTGGACCGGCGCGCTC	120	
DB	61	CTGTGCTATGGTCTCTGGCTGACTTTCGGGCGCGGTGTGGTACGCGTGGACCGGCGCGCTC	120	
QY	121	CGCTACGACCTGAGCGGCTTGGGCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCA	180	
DB	121	CGCTACGACCTGAGCGGCTTGGGCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCA	180	
QY	181	GCGCGGGGAGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCC	240	
DB	181	GCGCGGGGAGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCC	240	
QY	241	CTTCCGCCCGCGGTGTATCGAGAAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGA	300	
DB	241	CTTCCGCCCGCGGTGTATCGAGAAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGA	300	
QY	301	TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAGCTTCTGCGCGTT	360	
DB	301	TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAGCTTCTGCGCGTT	360	
QY	361	AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAG	420	
DB	361	AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAG	420	
QY	421	TGGTGAGAAATCCGTATGCCCCCTGAATCTCTGCGCTGACTTTGTGGTGGGCTTAT	480	
DB	421	TGGTGAGAAATCCGTATGCCCCCTGAATCTCTGCGCTGACTTTGTGGTGGGCTTAT	480	
QY	481	GTGTGCACTGGGCGATTATTAATGGCTCTTTTTCACCGCACACGACTGCAAGGCTCAGT	540	
DB	481	GTGTGCACTGGGCGATTATTAATGGCTCTTTTTCACCGCACACGACTGCAAGGCTCAGT	540	
QY	541	CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTTAAGTTCTTTTCTGTGAAAAC	600	
DB	541	CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTTAAGTTCTTTTCTGTGAAAAC	600	
QY	601	GAATTCGAGTCTGTGGGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT	660	
DB	601	GAATTCGAGTCTGTGGGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT	660	
QY	661	CTATACGACTTACAGGACAGAGATGGGGAATTCTATGGCTGTGTGGAGCAATGAACCCCA	720	
DB	661	CTATACGACTTACAGGACAGAGATGGGGAATTCTATGGCTGTGTGGAGCAATGAACCCCA	720	
QY	721	GTCTTACGAGCTGCTGATCAAGAGGCTTGGACTAAAGTCTGATGATCACTTCCCAATCAGAT	780	
DB	721	GTCTTACGAGCTGCTGATCAAGAGGCTTGGACTAAAGTCTGATGATCACTTCCCAATCAGAT	780	
QY	781	GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTTTCGAAAGAGAC	840	
DB	781	GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTTTCGAAAGAGAC	840	
QY	841	GAAGGAGAGTGGTCAAAATCTTTTGAACGCGACAGATGCTGTGTGACTCCGGTTCTGAC	900	
DB	841	GAAGGAGAGTGGTCAAAATCTTTTGAACGCGACAGATGCTGTGTGACTCCGGTTCTGAC	900	

Db	1621 A 1621	
RESULT 9		
ACAS9364	standard; cDNA; 1621 BP.	
ID	ACAS9364	
AC	ACAS9364;	
XX		
DT	10-JUN-2003 (first entry)	
XX		
DE	Prostate cancer therapy associated cDNA #107.	
XX		
KW	Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;	
KW	immunogen; cancer; prostate specific antigen; PSA;	
KW	prostatic acid phosphatase; PAP; prostate specific membrane antigen;	
KW	PSMA; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	US2002192763-A1.	
XX		
PD	19-DEC-2002.	
XX		
PF	29-JUN-2001; 2001US-00895793.	
XX		
PR	04-OCT-1999; 99US-0157455P.	
PR	04-OCT-2000; 2000US-00679272.	
PR	28-MAR-2001; 2001US-00822827.	
XX		
PA	(XUJ)/ XU J.	
PA	(DILL)/ DILLON D C.	
PA	(MITC)/ MITCHAM J L.	
PA	(HARL)/ HARLOCKER S L.	
PA	(JIAN)/ JIANG Y.	
PA	(KALO)/ KALOS M D.	
PA	(FANG)/ FANGER G R.	
PA	(RETT)/ RETTER M W.	
PA	(STOL)/ STOLK J A.	
PA	(DAYC)/ DAY C H.	
PA	(VEDV)/ VEDVICK T S.	
PA	(CART)/ CARTER D.	
PA	(LISX)/ LI S X.	
PA	(WANG)/ WANG A.	
PA	(SKEI)/ SKEIKY Y A W.	
PA	(HEPL)/ HEPLER W T.	
PA	(HEND)/ HENDERSON R A.	
PA	(HURA)/ HURAL J.	
PA	(MCNE)/ MCNEILL P D.	
PA	(HOUG)/ HOUGHTON R L.	
PA	(DBAS)/ Y DE BASSOLS C V.	
PA	(FOYT)/ FOY T M.	
XX		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;	
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,	
PI	Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA,	
PI	Mcneill PD, Houghton RL, Y De Bassols CV, Foy TM;	
XX		
DR	WPI; 2001-245062/25.	
XX		
PT	Prostate specific protein and its encoding polynucleotide, useful for the	
PT	treatment and diagnosis of prostate cancer.	
XX		
PS	Example 1; SEQ ID NO 107; 85pp; English.	
XX		
CC	The invention describes a fusion protein comprising at least one amino	
CC	acid sequence of immunogenic portions of any of the 3 sequences not	
CC	defined in the specification, or sequences having at least 70 or 90 %	
CC	sequence identity to any one of the 35 sequences defined in the USPTO web	
CC	site, which is encoded by any of the 4 nucleotide sequences not defined	
CC	in the specification. The fusion protein, composition and methods are	
CC	useful for diagnosing, preventing and/or treating cancer, particularly	

Qy	901	TTTTGAGAGGTTGTTTCATCATGATCAACAAGAAACGGGGTCGTTTATACACAGTGA	960
Db	901	TTTTGAGAGGTTGTTTCATCATGATCAACAAGAAACGGGGTCGTTTATACACAGTGA	960
Qy	961	GGAGCAGGACGTGAGCCCGCCCTGCCTCTGTAAACACCCAGCCCATCCCTTC	1020
Db	961	GGAGCAGGACGTGAGCCCGCCCTGCCTCTGTAAACACCCAGCCCATCCCTTC	1020
Qy	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT	1080
Db	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT	1080
Qy	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATAGGTAAA	1140
Db	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATAGGTAAA	1140
Qy	1141	AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAAATCTGCATTTACAGTG	1200
Db	1141	AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAAATCTGCATTTACAGTG	1200
Qy	1201	TAGAGTAAACACATAACATTTGATTCATCTGGAACAATGGAGGAACAGTATTACAGTGTCCTA	1260
Db	1201	TAGAGTAAACACATAACATTTGATTCATCTGGAACAATGGAGGAACAGTATTACAGTGTCCTA	1260
Qy	1261	CCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGATGAATTTCTAAA	1320
Db	1261	CCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGATGAATTTCTAAA	1320
Qy	1321	AATGGTTTACATTAAGGCGTTTGGATTTTATAAACTTTGGGTACTTATACATAATATGGT	1380
Db	1321	AATGGTTTACATTAAGGCGTTTGGATTTTATAAACTTTGGGTACTTATACATAATATGGT	1380
Qy	1381	AGTTATTCTGCCTTCCAGTTTGGCTTGATATATTTTGGTGAATTAAGATTTCTTGACTTATA	1440
Db	1381	AGTTATTCTGCCTTCCAGTTTGGCTTGATATATTTTGGTGAATTAAGATTTCTTGACTTATA	1440
Qy	1441	TTTTGGAATGGGTTCTAGTGAAAAAGGAATGATATATTTCTTGAAGACATTCGATATACATTT	1500
Db	1441	TTTTGGAATGGGTTCTAGTGAAAAAGGAATGATATATTTCTTGAAGACATTCGATATACATTT	1500
Qy	1501	ATTTTACACTCTTGATTTCTAGAACTGAGAAATGAGGAATGCCACAAATTTCTATGGTGAT	1560
Db	1501	ATTTTACACTCTTGATTTCTAGAACTGAGAAATGAGGAATGCCACAAATTTCTATGGTGAT	1560
Qy	1561	AAAAAGTCACGTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Db	1561	AAAAAGTCACGTGAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Qy	1621	A 1621	
		↓	
Db	1621	A 1621	

RESULT 10	
AAS10106	
ID	AAS10106 standard; cDNA; 1621 BP.
XX	
XX	
AC	AAS10106;
XX	
XX	24-OCT-2001 (first entry)
DT	
XX	
XX	Human prostate tumour cDNA F1-12 #3.
DE	
XX	
XX	Human; prostate tumour protein; prostate cancer; ss.
KW	
KW	
XX	
XX	Homo sapiens.
OS	
XX	
XX	US6262245-B1.
FN	
XX	
XX	17-JUL-2001.
PD	
XX	
XX	25-FEB-1998; 98US-00030607.
PF	
XX	
XX	

PR	25-FEB-1997;	97US-00806099.	
PR	01-AUG-1997;	97US-00904804.	
PR	09-FEB-1998;	98US-00020956.	
PA	(CORI-) CORIXA CORP.		
XX			
XX	Xu J, Dillon DC;		
XX	WPI; 2001-440862/47.		
DR	P-PSDB; AAU04959.		
DR			
XX			
XX	Novel polynucleotide encoding polypeptide comprising a portion of		
PT	prostate tumor protein useful for inhibiting development of prostate		
PT	cancer or for treating prostate cancer in a patient.		
XX			
PS	Claim 1; Col 112-113; 105pp; English.		
XX			
CC	The sequence is a human prostate tumour cDNA which encodes a partial		
CC	tumour protein. The DNA is useful for inhibiting the development of		
CC	prostate cancer or for treating prostate cancer in a patient		
XX			
SQ	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;		
	Query Match	100.0%;	Score 1621; DB 5; Length 1621;
	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 1621; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCCATGGCACTCGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTCCGCCCGGGCCCGGCTT	60
DB	1	CGCCATGGCACTCGAGGGCATCTCGGTCAATGAGAGCTGTCCGGCTGTCCGCCCGGGCCCGGCTT	60
QY	61	CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGTGTACGGCTGGACCGGCCCGGCTC	120
DB	61	CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGTGTACGGCTGGACCGGCCCGGCTC	120
QY	121	CCGCTACGACTGAGCCGCTTTGGGCCCGGGCAAGCGCTCCGTAGTGTCTGACCTTGAGCA	180
DB	121	CCGCTACGACTGAGCCGCTTTGGGGCGGGCAAGCGCTCCGTAGTGTGGAACCTTGAGCA	180
QY	181	GCCCGGGGAGCCGCGTGTCTGGCGCTCTGTGCAAGCGTTCGATGTCTGTCTGGAGCC	240
DB	181	GCCCGGGGAGCCGCGTGTCTGGCGCTCTGTGCAAGCGTTCGATGTCTGTCTGGAGCC	240
QY	241	CTTCCGCCCGGGTGTCAATGAGAAATCTCAGCTGGGCCCAAGATCTGCAGCGGGAAAA	300
DB	241	CTTCCGCCCGGGTGTCAATGAGAAATCTCAGCTGGGCCCAAGATCTGCAGCGGGAAAA	300
QY	301	TCCAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAGGAGCTTCTGCCGGTT	360
DB	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAGGAGCTTCTGCCGGTT	360
QY	361	AGCTGGCCACGATATCAACTATTTTGGCTTTGTTCAGGTGTTCTCTCAAAAAATTCGAGAAG	420
DB	361	AGCTGGCCACGATATCAACTATTTTGGCTTTGTTCAGGTGTTCTCTCAAAAAATTCGAGAAG	420
QY	421	TGTTGAAATCCGTTATGCCCGCTGAAATCTCTGGCTGACTTTTGCTGGTGGTCCCTTAT	480
DB	421	TGTTGAAATCCGTTATGCCCGCTGAAATCTCTGGCTGACTTTTGCTGGTGGTCCCTTAT	480
QY	481	GTGTGCACTGGGCATTAATATGGCTCTTTTGTGACCGCACAGCACTGCAAGGCTCAGGT	540
DB	481	GTGTGCACTGGGCATTAATATGGCTCTTTTGTGACCGCACAGCACTGCAAGGCTCAGGT	540
QY	541	CATTGTGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCA	600
DB	541	CATTGTGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCA	600
QY	601	GAAATCCAGTCTGTGGGAAGCACCTCCAGGACAGAAATGTTGATGGTGGAGCACCTTT	660
DB	601	GAAATCCAGTCTGTGGGAAGCACCTCCAGGACAGAAATGTTGATGGTGGAGCACCTTT	660
QY	661	CTATACGACTTACAGGACAGCATATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720

Db 661 CTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTCTGATCAAGGACTTGGACTAAGAGTCTGATGAACCTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTCTGATCAAGGACTTGGACTAAGAGTCTGATGAACCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAAGAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAAGAGAC 840
Qy 841 GAAGGAGAGTGTGTCAAACTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900
Db 841 GAAGGAGAGTGTGTCAAACTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900
Qy 901 TTTTGAAGGAGTTGTTTCATCATGATCACAACAGGAACGGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGAAGGAGTTGTTTCATCATGATCACAACAGGAACGGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCCGACCCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCCGACCCATCCCTTC 1020
Qy 1021 TTTCAAAGGGATCCTTTTATAGGAGAAACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
Db 1021 TTTCAAAGGGATCCTTTTATAGGAGAAACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTAGATATAAATCATTGAAGTAATAAGTAAA 1140
Db 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTAGATATAAATCATTGAAGTAATAAGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAACTACTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAACTACTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAAATTTGATGATGAAACATGAGGAGAAACAGTATTACAGTGCTTA 1260
Db 1201 TAGAGTAACACATAAATTTGATGATGAAACATGAGGAGAAACAGTATTACAGTGCTTA 1260
Qy 1261 CCACCTCTAATCAGAAAGAAATACAGACTCTGATTTCTACAGTGATGATTAATCTTAAA 1320
Db 1261 CCACCTCTAATCAGAAAGAAATACAGACTCTGATTTCTACAGTGATGATTAATCTTAAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGATTTATAAAACTTTGGGTACTTACTATAATTAATGAT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGATTTATAAAACTTTGGGTACTTACTATAATTAATGAT 1380
Qy 1381 AGTTATTTCCCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTTCCCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTACACTCTTGATTTCAATGTAGAAATGAGGAAATGCCACAAATTTGATGTGAT 1560
Db 1501 ATTTACACTCTTGATTTCAATGTAGAAATGAGGAAATGCCACAAATTTGATGTGAT 1560
Qy 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Db 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621

RESULT 11

ABL94927
ID ABL94927 standard; cDNA; 1621 BP.

XX
AC ABL94927;

XX

DT 19-JUL-2002 (first entry)
XX Human FI-12 cDNA sequence SEQ ID NO 107.
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
KW Homo sapiens.
XX OS
XX US2002022248-A1.
PN 21-FEB-2002.
XX 12-JAN-2001; 2001US-00759143.
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETI/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX Claim 1; SEQ ID NO 107; 87pp; English.
PS The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention
XX

SQ	Sequence	1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
	Query Match	100.0%; Score 1621; DB 6; Length 1621;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1621; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCCATGSCACTCGAGGSCATCTCGGTCAATCGAGCTGTCGGCCCTGGCCCGGCGCCGTT 60
DB	1	CGCCATGSCACTCGAGGSCATCTCGGTCAATCGAGCTGTCGGCCCTGGCCCGGCGCCGTT 60
QY	61	CTGTGCTATGTCCTGGCTGACTTCCTGGGGCGCGTGTGGTAGCGGTGAGACCGGCCGCTC 120
DB	61	CTGTGCTATGTCCTGGCTGACTTCCTGGGGCGCGTGTGGTAGCGGTGAGACCGGCCGCTC 120
QY	121	CCGCTACGATGTCAGCCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGAACCTGGAAGCA 180
DB	121	CCGCTACGATGTCAGCCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGAACCTGGAAGCA 180
QY	181	GCCGGGGAGCCGCGTCTGCGCGCTCTGTGCAAGCGGTCCGATGTGCTGGAGCC 240
DB	181	GCCGGGGAGCCGCGTCTGCGCGCTCTGTGCAAGCGGTCCGATGTGCTGGAGCC 240
QY	241	CTTCGCGCGCGTGTGTCAGAGAAACTCCAGCTGGGCCCAGAGATTCCTGACGCGGAAAA 300
DB	241	CTTCGCGCGCGTGTGTCAGAGAAACTCCAGCTGGGCCCAGAGATTCCTGACGCGGAAAA 300
QY	301	TCCAAGGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGAGAACTTCTCCCGGTT 360
DB	301	TCCAAGGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGAGAACTTCTCCCGGTT 360
QY	361	AGCTGGCCACCATATCAACTATTTGGCTTCTGCAAGCGGTCCGATGTGCTGGAGCC 420
DB	361	AGCTGGCCACCATATCAACTATTTGGCTTCTGCAAGCGGTCCGATGTGCTGGAGCC 420
QY	421	TGGTGAGAAATCCGTATGCCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGTCCCTTAT 480
DB	421	TGGTGAGAAATCCGTATGCCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGTCCCTTAT 480
QY	481	GTGTGCACTGGGCATTAATAATGGCTCTTTTGAACGCAACGCACTGACAAAGGTTCAGGT 540
DB	481	GTGTGCACTGGGCATTAATAATGGCTCTTTTGAACGCAACGCACTGACAAAGGTTCAGGT 540
QY	541	CATTGATCAATATGGTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600
DB	541	CATTGATCAATATGGTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600
QY	601	GAATTCGAGTCTGTGGGAGCACTTCGAGGACAGAACTTGTGGATGGTGAGCACCTTT 660
DB	601	GAATTCGAGTCTGTGGGAGCACTTCGAGGACAGAACTTGTGGATGGTGAGCACCTTT 660
QY	661	CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
DB	661	CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
QY	721	GTTCTACAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780
DB	721	GTTCTACAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780
QY	781	GAGCATGATGATGGCCAGAAATCAAGAAAGTTCAGATGTATTTGCAAGAAAGAC 840
DB	781	GAGCATGATGATGGCCAGAAATCAAGAAAGTTCAGATGTATTTGCAAGAAAGAC 840
QY	841	GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATCCCTGTGTGACTCCGGTTCTGAC 900
DB	841	GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATCCCTGTGTGACTCCGGTTCTGAC 900
QY	901	TTTTTTCAGGAGTGTTCATCATGATCAACAAGGAAAGGGGCTCGTTTATCACCAGTGA 960
DB	901	TTTTTTCAGGAGTGTTCATCATGATCAACAAGGAAAGGGGCTCGTTTATCACCAGTGA 960
QY	961	GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCCGACCTCCCTTC 1020
DB	961	GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCCGACCTCCCTTC 1020

QY	1021	TTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
DB	1021	TTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATT 1080
QY	1081	CAGCCGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
DB	1081	CAGCCGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
QY	1141	AGCTAGTCTCTAACTTCAGGCCCAAGGCTCAAGTGAATTTGAAATCTGCAATTACAGTG 1200
DB	1141	AGCTAGTCTCTAACTTCAGGCCCAAGGCTCAAGTGAATTTGAAATCTGCAATTACAGTG 1200
QY	1201	TAGAGTAAACACATAAATGTCATGCGAATGGAACATGCGAGAACAGTATTAACAGTGTCTTA 1260
DB	1201	TAGAGTAAACACATAAATGTCATGCGAATGGAACATGCGAGAACAGTATTAACAGTGTCTTA 1260
QY	1261	CCACTCTAAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
DB	1261	CCACTCTAAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
QY	1321	AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTTGGGTACTTATACATAAATATGGT 1380
DB	1321	AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTTGGGTACTTATACATAAATATGGT 1380
QY	1381	AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTTATA 1440
DB	1381	AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTTATA 1440
QY	1441	TTTTGAATGGGTTCTAGTGAAAAGGAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
DB	1441	TTTTGAATGGGTTCTAGTGAAAAGGAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
QY	1501	ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCCAAAATTTGTATGGTGAT 1560
DB	1501	ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCCAAAATTTGTATGGTGAT 1560
QY	1561	AAAAGTCACTGGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
DB	1561	AAAAGTCACTGGAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
QY	1621	A 1621
DB	1621	A 1621
RESULT 12		
ABS58636		
ID	ABS58636	standard; cdna; 1621 BP.
XX	AC	ABS58636;
XX	DT	05-NOV-2002 (first entry)
XX	XX	Prostate tumour cdna #107.
XX	DE	Human; prostate tumour; immunotherapy; prostate cancer; gene; ss.
XX	KW	Homo sapiens.
XX	OS	US2002081580-A1.
XX	PN	27-JUN-2002.
XX	PD	25-FEB-1998; 98US-00030606.
XX	PF	25-FEB-1997; 97US-00806596.
XX	PR	01-AUG-1997; 97US-00904809.
XX	PR	09-FEB-1998; 98US-00020747.
XX	XX	(XUJ/) XU J.
XX	PA	(DILL/) DILLON D C.
XX	XX	

PI Xu J, Dillon DC;
XX WPI; 2002-607662/65.
XX Detecting prostate cancer comprises contacting a sample with an agent
PT capable of binding to a polypeptide with an immunogenic portion of a
PT prostate protein, oligonucleotide primers or a probe specific for DNA
PT encoding the polypeptide.
XX Claim 1; Page 59-60; 11pp; English.
XX The invention relates to a method of detecting prostate cancer by
CC contacting a biological sample from a patient with: (a) a binding agent
CC that binds to a polypeptide having an immunogenic portion of a prostate
CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the
CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);
CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the
CC polypeptide of (a). The method and polypeptides are useful for
CC diagnosing, treating, particularly by immunotherapy, monitoring the
CC progression, and inhibiting the development of prostate cancer in a
CC patient. The polypeptides may be used to generate antibodies useful for
CC the diagnosis and monitoring of prostate cancer. ABS58530-ABS58746
CC represent human prostate tumour cDNA sequences of the invention
XX SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 100.0%; Score 1621; DB 6; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCATGGCAGTGCAGGGGATCTCGGTCTATGGAGTGTCCGGCTCGCCCGGGCCCGGT 60
DB 1 CGCCATGGCAGTGCAGGGGATCTCGGTCTATGGAGTGTCCGGCTCGCCCGGGCCCGGT 60
QY 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCGGTGTGGTACGGGTGGACCGGGCCCGCTC 120
DB 61 CTGTGCTATGTCCTGGCTGACTTTCGGGGCGGTGTGGTACGGGTGGACCGGGCCCGCTC 120
QY 121 CGCTACGACGTGAGCGGCTTGGCGGGCGAGCGCTCGTAGTCTGAGCTGAGCA 180
DB 121 CGCTACGACGTGAGCGGCTTGGCGGGCGAGCGCTCGTAGTCTGAGCTGAGCA 180
QY 181 GCGCGGGGAGCGCGGCTGTCGGCGGTCTGTGCAAGCGGTGCGATGTCGTGGAGCC 240
DB 181 GCGCGGGGAGCGCGGCTGTCGGCGGTCTGTGCAAGCGGTGCGATGTCGTGGAGCC 240
QY 241 CTTCCGCCCGGCTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCGACGGGAAA 300
DB 241 CTTCCGCCCGGCTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCGACGGGAAA 300
QY 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCGCCGTT 360
DB 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCGCCGTT 360
QY 361 AGCTGCCACGATATCACTATTGTCGTCAGGTGTTCTCTCAAAAATTGGCAGAG 420
DB 361 AGCTGCCACGATATCACTATTGTCGTCAGGTGTTCTCTCAAAAATTGGCAGAG 420
QY 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTCGGCTGACTTTGTCGGTGGCTTAT 480
DB 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTCGGCTGACTTTGTCGGTGGCTTAT 480
QY 481 GTGTGACATGGGATTTATATGGCTCTTTTGGCCGACACGACTGACAGGGTCAGGT 540
DB 481 GTGTGACATGGGATTTATATGGCTCTTTTGGCCGACACGACTGACAGGGTCAGGT 540
QY 541 CATTGATGCAATATGCTGGAAGAACACATATTTAAGTCTTTCTGTGGAATACTCA 600
DB 541 CATTGATGCAATATGCTGGAAGAACACATATTTAAGTCTTTCTGTGGAATACTCA 600
QY 601 GAAATCGAGTCTGTGGGAGGACCTCGAGGACAGAACTGTTGGATGGTGAGCACTTT 660
DB 601 GAAATCGAGTCTGTGGGAGGACCTCGAGGACAGAACTGTTGGATGGTGAGCACTTT 660

RESULT 13
ACC95091
ID ACC95091 standard; cDNA; 1621 BP.

QY 661 CTATACGACTTACAGCAGCAGATGGGGAATTCATGGCTGTTGGCAATAGAACCCCA 720
DB 661 CTATACGACTTACAGCAGCAGATGGGGAATTCATGGCTGTTGGCAATAGAACCCCA 720
QY 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGAGCTAAAGTCTGATGAATTTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGAGCTAAAGTCTGATGAATTTCCCAATCAGAT 780
QY 781 GAGCATGATGATTCGCCAGAAATGAAGAAGTTCGAGATGATTTTTCGAAAGAAC 840
DB 781 GAGCATGATGATTCGCCAGAAATGAAGAAGTTCGAGATGATTTTTCGAAAGAAC 840
QY 841 GAAGCAGAGTGGTCTCAAAATCTTTGACGGCAGACAGATGCTGTGACTCCGGTTCCTGAC 900
DB 841 GAAGCAGAGTGGTCTCAAAATCTTTGACGGCAGACAGATGCTGTGACTCCGGTTCCTGAC 900
QY 901 TTTTTCAGGAGTGTTCATCATGATCAACAAGGAAAGGGCTCGTTTATCACCAGTGA 960
DB 901 TTTTTCAGGAGTGTTCATCATGATCAACAAGGAAAGGGCTCGTTTATCACCAGTGA 960
QY 961 GGAGCAGGACGTGAGCCCCCGCCCTGCTGCTGTTAAACACCCGAGCCATCCCTTC 1020
DB 961 GGAGCAGGACGTGAGCCCCCGCCCTGCTGCTGTTAAACACCCGAGCCATCCCTTC 1020
QY 1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
DB 1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
QY 1081 CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGATAA 1140
DB 1081 CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGATAA 1140
QY 1141 AGCTAGTCTCTAACTTCCAGGCCCGCGCTCAAGTCAATTTGAAATCTGCAATTTACAGTG 1200
DB 1141 AGCTAGTCTCTAACTTCCAGGCCCGCGCTCAAGTCAATTTGAAATCTGCAATTTACAGTG 1200
QY 1201 TAGAGTAAACATAATCTGATGCAATGGAACATGGAGAACAGATTTACAGTGTCTTA 1260
DB 1201 TAGAGTAAACATAATCTGATGCAATGGAACATGGAGAACAGATTTACAGTGTCTTA 1260
QY 1261 CCACCTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
DB 1261 CCACCTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
QY 1321 AATGTTTATCATAGGGCTTTTGAATTTATAAACTTTGGGTACTTTACTATAATTTATGTT 1380
DB 1321 AATGTTTATCATAGGGCTTTTGAATTTATAAACTTTGGGTACTTTACTATAATTTATGTT 1380
QY 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTTAAGATTTCTTGACTTATA 1440
DB 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTGTTGATATTTAAGATTTCTTGACTTATA 1440
QY 1441 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGGAAGACATCGATATACATTT 1500
DB 1441 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGGAAGACATCGATATACATTT 1500
QY 1501 ATTTACACTTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTGATGTTGAT 1560
DB 1501 ATTTACACTTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTGATGTTGAT 1560
QY 1561 AAAAGTCAAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
DB 1561 AAAAGTCAAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
QY 1621 A 1621
DB 1621 A 1621

Db 1381 AGTTATCTGCCTCCAGTTTGCTTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440
QY 1441 TTTTGAATGGTCTTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
QY 1501 ATTTACACTCTTGATCTTCAATGTAGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560
Db 1501 ATTTACACTCTTGATCTTCAATGTAGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560
QY 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
Db 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
QY 1621 A 1621
Db 1621 A 1621
RESULT 14
ADBI3557
ID ADBI3557 standard; cDNA; 1621 BP.
XX ADBI3557;
AC ADBI3557;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific full length cDNA F1-12/P504S.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
PA (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Kalos MD;
PI WPI: 2003-756193/71.
XX P-PSDB; ADBI3558.
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Claim 19; Page; 101pp; English.
XX
CC The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is one of the
CC disclosed human prostate specific cDNAs. Note: Except where otherwise
CC indicated, the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 100.0%; Score 1621; DB 10; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCATGGCAGCTGAGGGCATCTCGGTCTATGAGCTGTCCGGCTTGGCCCGCCGCGCTT 60
Db 1 CGCCATGGCAGCTGAGGGCATCTCGGTCTATGAGCTGTCCGGCTTGGCCCGCCGCGCTT 60
QY 61 CTGTGCTATGTCCTGGTGTGACTTCGGGGCGCGTGTGTGTACGCTGTGACCGCGCCGCTC 120
Db 61 CTGTGCTATGTCCTGGTGTGACTTCGGGGCGCGTGTGTGTACGCTGTGACCGCGCCGCTC 120
QY 121 CCGCTACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAGCA 180
Db 121 CCGCTACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAGCA 180
QY 181 GCCCGGGGAGCGCCGCTGTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGTGAGCC 240
Db 181 GCCCGGGGAGCGCCGCTGTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGTGAGCC 240
QY 241 CTTCCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGACGGGAAA 300
Db 241 CTTCCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGACGGGAAA 300

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QY 301 TCCAAAGCTTATTTATGCGCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
Db 301 TCCAAAGCTTATTTATGCGCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
QY 361 AGCTGGCCACAGATACAACATAATTTGGCTTTGTGTCAGGTCTCTCAAAAATTTGCAGAA 420
Db 361 AGCTGGCCACAGATACAACATAATTTGGCTTTGTGTCAGGTCTCTCAAAAATTTGCAGAA 420
QY 421 TGGTGAGAAATCCGATATGCCCCGCTGAATCTCTCGCTGACCTTTGCTGGTGGTCCCTTAT 480
Db 421 TGGTGAGAAATCCGATATGCCCCGCTGAATCTCTCGCTGACCTTTGCTGGTGGTCCCTTAT 480
QY 481 GTGTGCACTGGGCATTAATAATGGCTCTTTTGAACCGCAACAGCACTGCAAGGGTCAGGT 540
Db 481 GTGTGCACTGGGCATTAATAATGGCTCTTTTGAACCGCAACAGCACTGCAAGGGTCAGGT 540
QY 541 CATTGATCAAAATATGGTGGGAAGGACAGCATATTTAAGTTCTTTCTGTGGAACCTCA 600
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Db 901 TTTTGAGGAGTGTGTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACAGTGA 960
QY 961 GGAGCAGCAGTGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020
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Db 1021 TTTCAAAAGGGATCCTTTATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATT 1080
QY 1081 CAGCCGCGAAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140
Db 1081 CAGCCGCGAAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140
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QY 1501 ATTTACACTCTTGATTTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1560
Db 1501 ATTTACACTCTTGATTTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1560
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Db 1561 AAAAGTCACCTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
QY 1621 A 1621
Db 1621 A 1621

RESULT 15
ADG26973
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XX AC ADG26973;
XX DT 26-FEB-2004 (first entry)
XX DE Human prostate-specific cDNA #107.
XX KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
XX OS Homo sapiens.
XX PN US2003157089-A1.
XX PD 21-AUG-2003.
XX PF 09-MAY-2002; 2002US-00144678.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 09-FEB-1998; 98US-00020956.
XX PR 25-FEB-1998; 98US-00030607.
XX PR 14-JUL-1998; 98US-00115453.
XX PR 23-SEP-1998; 98US-00159812.
XX PR 15-JAN-1999; 99US-00232149.
XX PR 09-APR-1999; 99US-00288946.
XX PR 13-JUL-1999; 99US-00352616.
XX PR 12-NOV-1999; 99US-00439313.
XX PR 18-NOV-1999; 99US-00443686.
XX PR 14-JAN-2000; 2000US-00483672.
XX PR 27-MAR-2000; 2000US-00536857.
XX PR 09-MAY-2000; 2000US-00568100.
XX PR 12-MAY-2000; 2000US-00570737.
XX PR 13-JUN-2000; 2000US-00593793.
XX PR 27-JUN-2000; 2000US-00605783.
XX PR 09-AUG-2000; 2000US-00636215.
XX PR 29-AUG-2000; 2000US-00651236.
XX PR 06-SEP-2000; 2000US-00657279.
XX PR 02-OCT-2000; 2000US-00679426.
XX PR 10-OCT-2000; 2000US-00685166.
XX PR 09-NOV-2000; 2000US-00709729.
XX PR 12-JAN-2001; 2001US-00759143.
XX PR 09-FEB-2001; 2001US-00780669.
XX PR 29-MAY-2001; 2001US-00852911.
XX PR 29-JUN-2001; 2001US-00895814.
XX PR 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.
XX PA
XX
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PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX
WI: 2003-777973/73.
DR P-PSDB; ADG25974.
XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 1; SEQ ID NO 107; 99pp; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 1621; DB 10; Length 1621;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGGCATCTCGGTCTATGAGCTGTCCGCCCTGGCCCGGGCCGGTT 60
DB 1 CGCCATGGCACTGCAGGGCATCTCGGTCTATGAGCTGTCCGCCCTGGCCCGGGCCGGTT 60

QY 61 CTGTGCTATGCTCTGGCTGACTTGGGGGGGGTGTGTGACGCTGGACCGGCCGGCTC 120
DB 61 CTGTGCTATGCTCTGGCTGACTTGGGGGGGGTGTGTGACGCTGGACCGGCCGGCTC 120

QY 121 CGCTACGACGTCAGCGGCTTGGCCGGGCAAGCGCTCGCTAGTGTGCGACCTGAAGCA 180
DB 121 CGCTACGACGTCAGCGGCTTGGCCGGGCAAGCGCTCGCTAGTGTGCGACCTGAAGCA 180

QY 181 GCGCGGGGAGCGCGGCTGCTCGGCGTCTGTGCAAGCGGTGCGATGCTGCTGAGCC 240
DB 181 GCGCGGGGAGCGCGGCTGCTCGGCGTCTGTGCAAGCGGTGCGATGCTGCTGAGCC 240

QY 241 CTTTCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGGA 300
DB 241 CTTTCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGGA 300

QY 301 TCCAGGCTTATTTATGCGAGCTCAGTGGATTTGGCCAGTCAGAGCTTCGCGGTT 360
DB 301 TCCAGGCTTATTTATGCGAGCTCAGTGGATTTGGCCAGTCAGAGCTTCGCGGTT 360

QY 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGA 420
DB 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGA 420

QY 421 TGGTGAGAAATCGTATGCCCCGCTGAATCTCTGCGTGAATTTGCTGTGTTGCTTAT 480
DB 421 TGGTGAGAAATCGTATGCCCCGCTGAATCTCTGCGTGAATTTGCTGTGTTGCTTAT 480

QY 481 GTGTGACCTGGCATTTATATGCTCTTTTTCACCGCACACGACTGCAAGGGTCAGGT 540
DB 481 GTGTGACCTGGCATTTATATGCTCTTTTTCACCGCACACGACTGCAAGGGTCAGGT 540

QY 541 CATTGATGCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 600

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QY 781 GAGCATGATGATGGCCAGAAATGAAGAAGAGTTTCAGATGATTTGCAAAAGAAC 840
DB 781 GAGCATGATGATGGCCAGAAATGAAGAAGAGTTTCAGATGATTTGCAAAAGAAC 840
QY 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
DB 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGAC 900
QY 901 TTTTGGAGAGTGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTATCACAGTGA 960
DB 901 TTTTGGAGAGTGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTATCACAGTGA 960
QY 961 GGAGCAGACCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
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QY 1621 A 1621
DB 1621 A 1621

Search completed: December 31, 2006, 12:54:19
Job time : 1261.98 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:14:13 ; Search time 5186.18 Seconds
(without alignments)
6976.201 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattatcatgta.....acttgataaaggaccggt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	427.8	66.2	478	1	AI732098
2	411.2	63.7	461	1	AA225199
3	376.6	58.3	447	1	AI732238
4	373.8	57.9	480	2	BF855163
5	373.6	57.8	447	4	EX096004
6	359.6	55.7	500	1	AA225313
7	356.4	55.2	541	11	AQ545351
8	355	55.0	456	1	AI734072
9	353.8	54.8	546	11	AQ469231
10	335.8	52.0	713	14	AG183700
11	313.6	48.5	533	12	CG891636
12	298.8	46.3	481	11	AQ199998
13	292.2	45.2	474	11	AQ171162
14	241.4	37.4	578	11	AQ726978
15	232.2	35.9	407	11	AQ598346
16	221.6	34.3	767	7	BF679787
17	216.2	33.5	698	7	BF676535
18	212.2	32.8	374	1	AA639908
19	202	31.3	578	9	DA878876

20	186	28.8	560	9	DA868489
C 21	177.2	27.4	234	1	AA579128
22	168.6	26.1	1512	2	BF965166
C 23	112.4	17.4	397	1	AA507792
24	101.4	15.7	683	2	EG924354
25	97	15.0	784	11	AQ782590
26	92.4	14.3	475	11	AQ496973
27	77.2	12.0	716	14	AG179840
C 28	66	10.2	369	2	BG998422
29	63	9.8	76	14	AG187983
C 30	54	8.4	310	7	BE142028
C 31	53.8	8.3	466	12	CE814791
32	53.8	8.3	674	12	CE482447
33	53.8	8.3	762	12	CE283656
C 34	53.4	8.3	272	7	BE168137
C 35	52.8	8.2	407	8	CV317561
C 36	51.4	8.0	343	1	AI672225
37	51.2	7.9	394	7	BF368099
C 38	50.2	7.8	861	12	BZ874654
C 39	49.8	7.7	644	14	AGO38156
C 40	49	7.6	300	7	BF368114
41	47	7.3	818	14	CT386427
42	47	7.3	877	14	CT109462
43	46.8	7.2	836	9	DN287707
C 44	46.8	7.2	860	9	DN288889
45	46.4	7.2	883	12	CC576958

ALIGNMENTS

RESULT 1
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LOCUS nc22g03.x5 NCI_CGAP_Prl1 Homo sapiens cdna clone IMAGE:1008916, mRNA
DEFINITION sequence.
ACCESSION AI732098
VERSION AI732098.1 GI:5053233
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 478)
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI EST Project
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40UP from Gibco
High quality sequence stop: 431.

FEATURES
Location/Qualifiers
1..478
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1008916"
/sex="Male"

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/dev stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Prl"
/notes="Vector: PAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

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ORIGIN

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Query Match      66.2%; Score 427.8; DB 1; Length 478;
Best Local Similarity 97.6%; Pred. No. 5.4e-117;
Matches 456; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

QY 137 GATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTGCCACCCCTCTGACCCCT 196
Db 9 GATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTGCCACCCCTCTGACCCCT 68

QY 197 TTGGAACTCCTTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTAGAGAAAGACCAA 256
Db 69 TTGGAACTCCTTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTAGAGAAAGACCAA 128

QY 257 CAACGGCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 316
Db 129 CAACGGCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 188

QY 317 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCATTTTGTGTGGAT 376
Db 189 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCATTTTGTGTGGAT 248

QY 377 AAAGTCAGAGTCCCGAGGGCCAGAGCAGGGGGCTTGTGTTGGGAACAATGGCTGAG 436
Db 249 AAAGTCAGAGTCCCGAGGGCCAGAGCAGGGGGCTTGTGTTGGGAACAATGGCTGAG 307

QY 437 CATATAACCATAGGTTATGGGGAACAAACAAACATCAAAAGTCACCTGTATCAATTTGCCATG 496
Db 308 CATATAACCATAGGTTATGGGGAACAAACAAACATCAAAAGTCACCTGTATCAATTTGCCATG 364

QY 497 AAGACTTGAGGACCTGTAATCTACCGATTCATCTTAAGGACAGCAGGACGAGTTGAGTGG 556
Db 365 AAGACTTGAGGACCTGTAATCTACCGATTCATCTTAAGGACAGCAGGACGAGTTGAGTGG 424

QY 557 CAACAATGCAGCAGCAGATCAATCGAAGAACACACAGAAATGATGCAAT 603
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RESULT 2
AA225199
LOCUS nc22g03.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008916, mRNA
DEFINITION
ACCESSION AA225199
VERSION AA225199.1 GI:1846507
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 461)
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```

```

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -41m13 fwd. Ef from Amersham
High quality sequence stop: 367.
Location/Qualifiers
source
1. .461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1008916"
/sex="Male"
/dev stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Prl"
/notes="Vector: PAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

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FEATURES

source

ORIGIN

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Query Match      63.7%; Score 411.2; DB 1; Length 461;
Best Local Similarity 96.5%; Pred. No. 5.3e-112;
Matches 440; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 137 GATCTGTAGCAAGAGAAACAAACACTGATCTCTTTCTGCCACCCCTCTGACCCCT 196
Db 1 GATCTGTAGCAAGAGAAACAAACACTGATCTCTTTCTGCCACCCCTCTGACCCCT 60

QY 197 TTGGAATCTCTTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTAGAGAAAGACCAA 256
Db 61 TTGGAATCTCTTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTAGAGAAAGACCAA 120

QY 257 CAACGGCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 316
Db 121 CAACGGCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 180

QY 317 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCATTTTGTGTGGAT 376
Db 181 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCATTTTGTGTGGAT 240

QY 377 AAAGTCAGAGTCCCGAGGGCCAGAGCAGGGGGCTTGTGTTGGGAACAATGGCTGAG 436
Db 241 AAAGTCAGAGTCCCGAGGGCCAGAGCAGGGGGCTTGTGTTGGGAACAATGGCTGAG 299

QY 437 CATATAACCATAGGTTATGGGGAACAAACAAACATCAAAAGTCACCTGTATCAATTTGCCATG 496
Db 300 CATATAACCATAGGTTATGGGGAACAAACAAACATCAAAAGTCACCTGTATCAATTTGCCATG 356

QY 497 AAGACTTGAGGACCTGTAATCTACCGATTCATCTTAAGGACAGCAGGACGAGTTGAGTGG 556
Db 357 AAGACTTGAGGACCTGTAATCTACCGATTCATCTTAAGGACAGCAGGACGAGTTGAGTGG 416

QY 557 CAACAATGCAGCAGCAGATCAATCGAAGAACACACAGAAATGATGCAAT 592
Db 417 CAACAATGCAGCAGCAGATCAATCGAAGAACACACAGAAATGATGCAAT 452

```

RESULT 3

AI732238/c

LOCUS

AI732238

447 bp

mRNA

linear

EST 13-DEC-1999

DEFINITION nf31901.x5 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:915408 similar to contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AI732238

VERSION AI732238.1 GI:50533351

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 447)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

This read has been verified (found to hit its original self in the correct orientation)

Insert Length: 621 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 423.

FEATURES

source
1. .447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:915408"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Prl"
/notes="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

ORIGIN

Query Match 58.3%; Score 376.6; DB 1; Length 447;
Best Local Similarity 95.7%; Pred. No. 1.4e-101;
Matches 420; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

QY 178 CTGCCACCCCTCGACCCCTTGGAACTCTCTGACCTTTAGAACAGGCTTACCTAATAT 237
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DB 447 CTGCCACCCCTCGACCCCTTGGAACTCTCTGACCTTTAGAACAGGCTTACCTAATAT 388
|||||

QY 238 CTGCTAGAGAAAGACCAACAGCGCTCAAGAGTCTCTTACCATGAAGGCTCAGCTA 297
|||||

DB 387 CTGCTAGAGAAAGACCAACAGCGCTCAAGAGTCTCTTACCATGAAGGCTCAGCTA 328
|||||

QY 298 ATTCTTGGCTAAGATGTGGGTTCACATTAGGTTCTGAATATGGGGGAA-GGGTCAATT 356
|||||

DB 327 ATTCTTGGCTAAGATGTGGGTTCACATTAGGTTCTGAATATGGGGGAAAGGGTCAATT 268
|||||

QY 357 TGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTG 416
|||||

DB 267 TGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTG 209
|||||

QY 417 CTTTGGGAACAATGGCTGAGCATATAACCATAGGTATATGGGAACAAACACATCAAG 476
|||||

DB 208 CTTTGGGAACAATGGCTGAGCATATAACCATAGG---TATGGGAACAAAAACATCAAG 152
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QY 477 TCACGTGATCAATTCCTATGAAGACTTGAGGACCTGAACTTACCGATTCACTTAAAGC 536
|||||

DB 151 TCACGTGATCAATTCCTATGAAGACTTGAGGACCTGAACTTACCGATTCACTTAAAGC 92
|||||

QY 537 AGCAGGACCAAGTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAAACAGAAATGA 596
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DB 91 AGCAGGACCAAGTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAAACAGAAATGA 32
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QY 597 TTGCAATGTCCTTTTTTTT 615
|||||

DB 31 TTGCAATCATCTCTGTGTT 13
|||||

RESULT 4

BF855163/c
LOCUS RC3-FN0201-111100-011-f05 FN0201 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF855163
VERSION BF855163.1 GI:12242907
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)

REFERENCE 1
AUTHORS Dias Neto,S., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zaglo,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3&t2=RC3-FN0201-111100-011-f05&t3=2000-11-11&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 478.
Location/Qualifiers
1. .480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0201"
/note="Organ: prostate normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source
1. .480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0201"
/note="Organ: prostate normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

REFERENCE 1 (bases 1 to 500)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 rev1 BT from Amersham
High quality sequence stop: 367.

FEATURES
source
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1008916"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr1"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN

Query Match 55.7%; Score 359.6; DB 1; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.8e-96;
Matches 458; Conservative 0; Mismatches 15; Indels 10; Gaps 8;

QY 137 GATCTGGTAGCAAA-GAAGAGAAACAACACATGATCTCTTTCGCCACCCCTCTGA-CC 194
DB 485 GATCTGGTAGCAAA-GAAGAGAAACAACACATGATCTCTTTCGCCACCCCTCTGA-CC 426

QY 195 CTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTCTAGAGAAAGACC 254
DB 425 CTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTCTAGAGAAAGACC 366

QY 255 AACACGGCC-TCAAGAGATCTTTACCATGAAGTCT-CAGCTAATCTTGGCTAAGAT 312
DB 365 AACACGGCCCTTCAAGAGATCTTTACCATGAAGTCTCAGCTAATCTTGGCTAAGAT 306

QY 313 GTGGGTTCACATTAGTGTCTGAATATGGGGGAGGCTCAATTTCTATTTTGTGTC 372
DB 305 GTGGGTTCACATTAGTGTCTGAATATGGGGGAGGCTCAATTTCTATTTTGTGTC 246

QY 373 GGATAAGTCAGGATGCCAGGGCCAGAGCAGGGGGCTGTGCTTGGGAACATGGC 432
DB 245 GGATAAGTCAGGAT-NCCAGGGGCCAGAGCAGGGGGCTGCTGCTTGGGAACATGGC 188

QY 433 TGAGCATATAACCATAGGTTATGGGAACAAACCAATCAAGTCACCTGTATCAATTC 492
DB 187 TGAGCATATAACCATAGG---TATGGGAACAAACCAATCAAGTCACCTGTATCAATTC 131

QY 493 CATGAAGACTTGGGACCTGAATCTACCGATTCATCTTAAGGCAGCAGACAGTTTGA 552
DB 130 CATGAAGACTTGGGACCTGAATCTACCGATTCATCTTAAGGCAGCAGACAGTTTGA 71

QY 553 GTGGCAACAATGCAGCAGCAGGAATCAATGGAAACAACAGATGATTGCAATGTCCTTTT 612

DB 70 GTGGCAACAATGCAGCAGCAGGAATCAAT-GAAACAACAGATGATTGCAATCTCTGT 12
QY 613 TTT 615
DB 11 GTT 9

RESULT 7
LOCUS AQ545351
DEFINITION CITBI-EI-2613A22.TF CITBI-EI Homo sapiens genomic clone 2613A22,
genomic survey sequence.
ACCESSION AQ545351
VERSION AQ545351.1 GI:4904594
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 541)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: CITBI-EI-2613A22.TP
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1..541
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2613A22"
/sex="male"
/cell_type="sperm"
/clone_lib="CITBI-EI"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

ORIGIN

Query Match 55.2%; Score 356.4; DB 11; Length 541;
Best Local Similarity 89.9%; Pred. No. 1.7e-95;
Matches 418; Conservative 0; Mismatches 37; Indels 10; Gaps 3;

QY 1 ACGATTTTCATTTATCATGTAAATCGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC 60
DB 81 ATGATTTTCATTTATCATGTAAATCGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC 140

QY 61 TGCTCAGGGGAGGTTTCATATGGGACTTTCTACTGCCAAGGTTCTATACAGGATATAA 120
DB 141 TGCT-TGGGGGAAGGCTCATATGGGACTTTCTACTGCCAAGGTTCTTACAGGATATAA 199

QY 121 GGGGCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAAACACTGATCTTTCTG 180
DB 200 GGTGCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAAACACTGATCTTTCTG 259

QY 181 CCACCCCTCTGACCTTTGGAACTCCTCTGACCCCTTTAGAACAGCTTACCTTAATCTG 240
DB 260 CCAC-----ATTATTGAACCCCTCTGACCCCTTTATAAACAAGCCACCTCATATCTG 311

ACCESSION CG891636
 VERSION CG891636.1 GI:51792549
 KEYWORDS GSS.
 SOURCE Pygathrix bieti (black snub-nosed monkey)
 ORGANISM Pygathrix bieti
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Colobinae; Pygathrix.
 1 (bases 1 to 533)
 Xu, H.L., Qian, Y.P., Yang, F.T., Nie, W.H., Chi, J.X. and Su, B.
 Construction and characterization of bacterial artificial
 chromosome (BAC) library of Yunnan snub-nosed monkey (*Rhinopithecus*
biети)
 Unpublished (2003)
 Contact: Xu, H.L.; Su, B.
 Key Laboratory of Cellular and Molecular Evolution
 Kunming Institute of Zoology, the Chinese Academy of Sciences
 32 Jiaochangdonglu, Kunming, Yunnan 650223, People's Republic of
 China
 Email: xuhl@mail.kiz.ac.cn
 Seq primer: 17
 Class: BAC ends.
 JOURNAL Location/Qualifiers
 COMMENT 1. 533
 /organism="Pygathrix bieti"
 /mol_type="genomic DNA"
 /strain="Yunnan snub-nosed monkey"
 /db_xref="taxon:61621"
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 /tissue_type="skin"
 /cell_type="Fibroblast"
 /cell_line="KCB96009"
 /clone_lib="Yunnan snub-nosed monkey genomic BAC library"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Genomic DNA was
 partially digested with EcoRI. Vector, pBACE3.6.
 Recombinants were transformed into DH10B."
 FEATURES source
 Location/Qualifiers
 1. 533
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7523108"
 /db_xref="taxon:9606"
 /clone="RPCI-11-61C21"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
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 Query Match 48.5%; Score 313.6; DB 12; Length 533;
 Best Local Similarity 83.8%; Pred. No. 1.3e-82;
 Matches 394; Conservative 0; Mismatches 61; Indels 15; Gaps 3;
 QY 68 GGAAGGTTTCATATGGGACTTCTACTGCCAAGGTTCTATACAGGATATAAGNGCCT 127
 DB 12 GGAAGGTTTCATATGGGACTTCTACTGCCAAGGTTCTATACAGGATATAAGTACCT 71
 QY 128 CACAGTATAGTCTGTAGCAAGAGAAAGAAACAAACACTGATCTCTTTCTGCCACCCC 187
 DB 72 CACAGTACAGATCTGTAGCAAGAGAGAAACAAACGCTGATCTCTTTCTGCCA---- 127
 QY 188 TCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCTACCTAATATCTGCTAGAGA 247
 DB 128 ----TTTATTGTGAACCCCTCTGACCCCTTTAGAACAGTGAATTAATCTGCTAAAGA 183
 QY 248 AAGACCAACAAACGGCTCAAGGATCTTTACCATGAAGTCTCAGCTAATCTTGCT 307
 DB 184 AAGACCAACAAACGGCTCAAGGATCTCGTACCAATGAAGTCTCAGCTAATCTTGCT 243
 QY 308 AAGATGTGGTTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCTCAATTTG 367
 DB 244 AAGATGTGGTTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCTCAATTTG 303
 QY 368 TGTGTGGATAAGTACAGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTTGGGAACA 427
 DB 304 TGTGTGGATAAGGCGAGGATGCTCAGCGCCAGAGCAGGGTCTG-GTGCTTTGGGAACA 362
 QY 428 ATGGCTGAGCATATACCATTAAGTTATGG-----GGACAAACAAACATCAAGTCACT 481
 DB 363 ATGACTGAGCAATTAAGCATAGGAATGGGAACATACAAACATTTGAACCTTCAAGCCACT 422
 QY 482 GTATCAATTTGCCATGAAGACTTGGAGGACTTCAATCTTACCGATTTCATCTT 531

Db 423 GTATGACTTGCCATGAAGACTTGAGGACTCTGAATCAGTAAGGCGCATCTT 472
 RESULT 12
 LOCUS AQ199998
 DEFINITION RPCI11-61C21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-61C21,
 genomic survey sequence.
 ACCSSON AQ199998
 VERSION AQ199998.1 GI:3612197
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 481)
 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
 Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
 Use of human BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1998)
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Class: BAC ends.
 FEATURES Location/Qualifiers
 1. 481
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 /db_xref="GDB:7523108"
 /db_xref="taxon:9606"
 /clone="RPCI-11-61C21"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 ORIGIN
 Query Match 46.3%; Score 298.8; DB 11; Length 481;
 Best Local Similarity 89.6%; Pred. No. 3.6e-78;
 Matches 346; Conservative 0; Mismatches 29; Indels 11; Gaps 2;
 QY 4 ATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCAACAGCTGGAGCCACTGC 63
 DB 107 ATTTTCATTATCATGTAAATCACATCACTCAAGGGGCCAACCAACAGCTGGAGCCACTGC 166
 QY 64 TCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATAAGGN 123
 DB 167 TCAGGGGAAGTTTCATACGGGACTTTCTACTGCCCAAGTTCTATACAGGATATAAGGT 226
 QY 124 GCCTCAGATATACATCTGTTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTGCCA 183
 DB 227 GCCTCAGATATACATCTGTTAGCA---AAGAGAAACAGACTGACCTCTCTCTGCCA 283
 QY 184 CCCCTCTGACCCCTTTGGAACCTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTA 243
 DB 284 C-----ATTATTTGAACCCCTCTCACCCCTTTAGAACAGCCCTACCTAATCTGCCA 335
 QY 244 GAGAAAAAGACCAACAGGCTTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATCTTT 303
 DB 336 GAGAAAAAGACCAACAGGCTTCAAGGATCTTTTACCATGAAGGTTCTCAGCTAATCTCT 395


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QY 304 GGCTAAGATGTGGTTCCACATTAGTTCTGAATATGGGGGGAAGGTCATTTGCTCAT 363
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Db 396 GGCTAAGATGTGGTTCCACATTAGTTCTGAATATGGGGGGAAGGTCATTTGCTCAC 455
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QY 364 TTGTGTGTGGATAAAGTCAGGATGC 389
    |||||
Db 456 TCTGTGTGGGATAAAGTCAGGATGC 481
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RESULT 13
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LOCUS HS_3070_B1_B09_MF_CIT_Approved_Human_Genomic_Sperm_Library_D_Homo
DEFINITION sapiens genomic clone Plate=3070 Col=17 Row=D, genomic survey
sequence.
ACCESSION AQL711162.1 GI:3568529
VERSION AQL711162
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 474)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: D column: 17
Class: BAC ends
High quality sequence stop: 474.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="Plate=3070 Col=17 Row=D"
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/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

FEATURES
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1..474
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="Plate=3070 Col=17 Row=D"
/sex="male"
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/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 45.2%; Score 292.2; DB 11; Length 474;
Best Local Similarity 89.9%; Pred. No. 3.5e-76;
Matches 338; Conservative 0; Mismatches 29; Indels 9; Gaps 2;

QY 1 ACAGATTTTCATTATCATGTAAATCGGTCCTCAAGGGCCCAACACAGCTGGAGCCAC 60
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Db 107 ATGATTTTCATTATCATGTAAATCGATCACTCAAGGGCCCAACACAGCTGGAGCCAC 166
    |||||
QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGATATAA 120
    |||||
Db 167 TGCT-TGGGGAAGGCTCATATGGGACTTTCTACTGCTTAAGGTTCTACAGGATATAA 225
    |||||
QY 121 GGGGCTCTCAGTATAGTCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180
    |||||
Db 226 GGTGGCTCTACTGTGTAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 285
    |||||
QY 181 CCACCCCTCTGACCCCTTGGAATCTCTGACCCCTTTAGAACACAGGCTACCTAATATCTG 240
    |||||
Db 286 CCAC-----ATTATTTGAACCCCTCTGACCCCTTTATAACAAGCCCTCATATCTG 337
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```

```

QY 241 CTAGAGAAAAGCAACCAACGCGCTCAAGAGTCTCTTACCATGAAGGTCCTCAGCTAATT 300
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Db 338 CTAGAGAAAAGCAACCAACGCGCTCAAGAGTCTCTTACCATGAAGGTCCTCAGCTAATT 397
    |||||
QY 301 CTTGGCTAAGATGTGGTTCCACATTAGTTCTGAATATGGGGGGAAGGTCATTTGCT 360
    |||||
Db 398 CTTAGCTAAGATGTGGTTCCACATTATGCTCTGAATACAGGGAAGGTCATTTGCT 457
    |||||
QY 361 CATTTTGTGTGGAT 376
    |||||
Db 458 CACTTTGTGTGGAT 473
    |||||

RESULT 14
AQL726978
LOCUS HS_5416_B2_F06_T7A_RPCI-11_Human_Male_BAC_Library_Homo_sapiens
DEFINITION genomic clone Plate=992 Col=12 Row=L, genomic survey sequence.
ACCESSION AQL726978.1 GI:5486647
VERSION AQL726978
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 578)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 992 row: L column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 578.
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Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

FEATURES
source
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/organism="Homo sapiens"
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/sex="male"
/clone.lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

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Best Local Similarity 82.6%; Pred. No. 7.3e-61;
Matches 314; Conservative 0; Mismatches 57; Indels 9; Gaps 3;

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 Hominidae; Homo.
 1 (bases 1 to 407)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
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 High quality sequence stop: 407.
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source

/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"

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Query Match 35.9%; Score 232.2; DB 11; Length 407;
 Best Local Similarity 86.2%; Pred. No. 3.8e-58;
 Matches 294; Conservative 0; Mismatches 35; Indels 12; Gaps 3;
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 Db 254 C-----ATTATATGAACCCCTCTCACCCTTTATACAGCCCACTTAACATCTGCCA 305
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 Qy 304 GGCTTAAGATGGGTTTCCACATTAGGTTCTGAATATGGGG 344
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
7716.790 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgattttcattcatgtgta.....acttgataaaaggggacgt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 5: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	646	100.0	647	3	US-09-780-669-308 Sequence 308, App
3	646	100.0	647	3	US-09-822-827-308 Sequence 308, App
4	646	100.0	647	3	US-09-232-880-308 Sequence 308, App
5	646	100.0	647	3	US-09-895-793-308 Sequence 308, App
6	646	100.0	647	3	US-09-895-814-308 Sequence 308, App
7	646	100.0	647	6	US-10-012-896-308 Sequence 308, App
8	646	100.0	647	6	US-10-010-940-308 Sequence 308, App
9	646	100.0	647	7	US-10-144-678A-308 Sequence 308, App
10	646	100.0	647	7	US-10-294-025-308 Sequence 308, App
11	646	100.0	647	16	US-11-234-786-308 Sequence 308, App
12	600.8	93.0	2577	7	US-10-294-025-1034 Sequence 1034, App
13	599.2	92.8	1481	9	US-10-357-930-21476 Sequence 21476, A
14	599.2	92.8	1481	9	US-10-357-930-21536 Sequence 21536, A
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C 21	599.2	92.8	1481	9	US-10-357-930-27951	Sequence 27951, A
C 22	599.2	92.8	2577	3	US-09-759-143-552	Sequence 552, App
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C 41	434.2	67.2	668	4	US-09-925-065A-489987	Sequence 489987
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ALIGNMENTS

RESULT 1

US-09-759-143-308

; Sequence 308, Application US/09759143

; Patent No. US20020022248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Hitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John H.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 308

; LENGTH: 647

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(647)

; OTHER INFORMATION: n = A,T,C or G

; US-09-759-143-308

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Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jjiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaeir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: n = A, T, C or G
; US-09-780-669-308

Query Match 100.0%; Score 646; DB 3; Length 647;

Best Local Similarity 100.0%; Pred. No. 2.7e-201;

Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
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RESULT 3

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; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jjiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.534C1
;; CURRENT APPLICATION NUMBER: US/09/822,827
;; CURRENT FILING DATE: 2001-03-28
;; NUMBER OF SEQ ID NOS: 982
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 308
;; LENGTH: 647
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(647)
;; OTHER INFORMATION: n = A,T,C or G
US-09-822-827-308

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Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60

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QY 121 GNGGCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
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QY 301 CTTGGCTAAGATGTGGGTTCCAAATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAAGATGTGGGTTCCAAATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGTGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420
DB 361 CATTTTGTGTGTGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAGTCTAC 480
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAGTCTAC 480

QY 481 TGTATCAATTGGCAATGAAGCTTGAAGGACCTGAAATCTACCGATTCACTTAAGGCAGCA 540
DB 481 TGTATCAATTGGCAATGAAGCTTGAAGGACCTGAAATCTACCGATTCACTTAAGGCAGCA 540

QY 541 GGACCAAGTTTGAAGTGGCAACATGACAGCAGAGATCAATGGAACCAACAGATGATGTC 600
DB 541 GGACCAAGTTTGAAGTGGCAACATGACAGCAGAGATCAATGGAACCAACAGATGATGTC 600

QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATATAAGGGGACCGT 647
DB 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATATAAGGGGACCGT 647
```

RESULT 4
US-09-232-880-308
; Sequence 308, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn

;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
;; FILE REFERENCE: 210121.428C6
;; CURRENT APPLICATION NUMBER: US/09/232,880
;; CURRENT FILING DATE: 1999-01-15
;; NUMBER OF SEQ ID NOS: 338
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 308
;; LENGTH: 647
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(647)
;; OTHER INFORMATION: n = A,T,C or G
US-09-232-880-308

```
Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTTATACAGGATATAA 120
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTTATACAGGATATAA 120

QY 121 GNGGCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
DB 121 GNGGCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACTGATCTCTTTCTG 180

QY 181 CCACCCCTCGACCTCTTGGAACCTCTGACCCCTTTAGAACCAAGCCTACCTAAATATCG 240
DB 181 CCACCCCTCGACCTCTTGGAACCTCTGACCCCTTTAGAACCAAGCCTACCTAAATATCG 240

QY 241 CTAGAGAAAAGACCAACACGGCCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300
DB 241 CTAGAGAAAAGACCAACACGGCCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300

QY 301 CTTGGCTAAGATGTGGGTTCCAAATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAAGATGTGGGTTCCAAATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGTGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420
DB 361 CATTTTGTGTGTGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAGTCTAC 480
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAGTCTAC 480

QY 481 TGTATCAATTGGCAATGAAGCTTGAAGGACCTGAAATCTACCGATTCACTTAAGGCAGCA 540
DB 481 TGTATCAATTGGCAATGAAGCTTGAAGGACCTGAAATCTACCGATTCACTTAAGGCAGCA 540

QY 541 GGACCAAGTTTGAAGTGGCAACATGACAGCAGAGATCAATGGAACCAACAGATGATGTC 600
DB 541 GGACCAAGTTTGAAGTGGCAACATGACAGCAGAGATCAATGGAACCAACAGATGATGTC 600

QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATATAAGGGGACCGT 647
DB 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATATAAGGGGACCGT 647
```

RESULT 5
US-09-895-793-308
; Sequence 308, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

```
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATATATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATATATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Qy 181 CCACCCCTTGACCTTTGGAACTCTGACCCCTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTTGACCTTTGGAACTCTGACCCCTTAGAACAGCCCTACCTAATATCTG 240
Qy 241 CTAGAGAAAGCAACCAAGGCCTCAAGAGTCTCTTACCATGAAGTCTCAGCTAAT 300
Db 241 CTAGAGAAAGCAACCAAGGCCTCAAGAGTCTCTTACCATGAAGTCTCAGCTAAT 300
Qy 301 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Qy 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGGCTGCTTGCCTT 420
Db 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGGCTGCTTGCCTT 420
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACAAACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACAAACATCAAAAGTCAC 480

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATATATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATATATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Qy 181 CCACCCCTTGACCTTTGGAACTCTGACCCCTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTTGACCTTTGGAACTCTGACCCCTTAGAACAGCCCTACCTAATATCTG 240
Qy 241 CTAGAGAAAGCAACCAAGGCCTCAAGAGTCTCTTACCATGAAGTCTCAGCTAAT 300
Db 241 CTAGAGAAAGCAACCAAGGCCTCAAGAGTCTCTTACCATGAAGTCTCAGCTAAT 300
Qy 301 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Qy 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGGCTGCTTGCCTT 420
Db 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGGCTGCTTGCCTT 420
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACAAACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACAAACATCAAAAGTCAC 480
```

```
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTTAAGATCTGGTTCACATTAAGTTCCTGAATATGCGGGGAAGGCTCAATTTGCT 360
Db 301 CTTGGCTTAAGATCTGGTTCACATTAAGTTCCTGAATATGCGGGGAAGGCTCAATTTGCT 360
QY 361 CAFTTTTGTGTGGATAAAGTCAAGATGCGCCAGGGGCGAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CAFTTTTGTGTGGATAAAGTCAAGATGCGCCAGGGGCGAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTGTATGGGGAACAAACAACATCAAGTCCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGTGTATGGGGAACAAACAACATCAAGTCCAC 480
QY 481 TGTATCAATTTGCGATGAAGCTTGAAGGACCTCAATCTTACCGATTCTTAAAGGCGACA 540
Db 481 TGTATCAATTTGCGATGAAGCTTGAAGGACCTCAATCTTACCGATTCTTAAAGGCGACA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCGAGCAGCAAGATCAATGGAACAAACAGATGATTCG 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCGAGCAGCAAGATCAATGGAACAAACAGATGATTCG 600
QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
```

RESULT 7

US-10-012-896-308
; Sequence 308, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-308

Query Match 100.0%; Score 646; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGATTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACCAAGCTGGAGCCAC 60
Db 1 AGATTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACCAAGCTGGAGCCAC 60
QY 61 TCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGATATAAA 120
Db 61 TCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGATATAAA 120
QY 121 GGGGCTCAGATATAGATCTGGTAGCAAAAGAAAGAAACAAACACATGATCTCTTTCTG 180
Db 121 GGGGCTCAGATATAGATCTGGTAGCAAAAGAAAGAAACAAACACATGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTTAAGATGTTGGGTTTCCACATTAAGTCTCTGAATATGCGGGGAAGGCTCAATTTGCT 360
Db 301 CTTGGCTTAAGATGTTGGGTTTCCACATTAAGTCTCTGAATATGCGGGGAAGGCTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAAGATGCGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAAGATGCGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAAACCATTAGTGTATGGGGAACAAACAACATCAAGTCCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAAACCATTAGTGTATGGGGAACAAACAACATCAAGTCCAC 480
QY 481 TGTATCAATTTGCGATGAAGCTTGAAGGACCTGAATCTACCGATTCTCTTAAAGGCGACA 540
Db 481 TGTATCAATTTGCGATGAAGCTTGAAGGACCTGAATCTACCGATTCTCTTAAAGGCGACA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCGAGCAGCAAGATCAATGGAACAAACAGATGATTCG 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCGAGCAGCAAGATCAATGGAACAAACAGATGATTCG 600
QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
```

RESULT 8

US-10-010-940-308
; Sequence 308, Application US/10010940
; Publication No. US2003008062A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

```
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)-(647)
; OTHER INFORMATION: n = A,T,C or G
US-10-010-940-308

Query Match      100.0%; Score 646; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAACAAACACTGTCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAACAAACACTGTCTCTTTCTG 180

Qy 181 CCACCCCTCTGACCTTTGGAACTCTCTGACCTTTTGAACCAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCTTTGGAACTCTCTGACCTTTTGAACCAAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300

Qy 301 CTTGGCTTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGTAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGTAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480
Db 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480

Qy 481 TGTATCAATTGCGATGAAGCTTTGAGGACCTGAAATCTACCGATTCTCTTTAAGCAGCA 540
Db 481 TGTATCAATTGCGATGAAGCTTTGAGGACCTGAAATCTACCGATTCTCTTTAAGCAGCA 540

Qy 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGAAACAAACAGATGATTC 600
Db 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGAAACAAACAGATGATTC 600

Qy 601 AATGTCCTTTTTTTTCTCTGCTCTCTGACTTATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTCTCTGACTTATAAAGGGGACCGT 647
```

RESULT 9

```
US-10-144-678A-308
; Sequence 308, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

```
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-308
```

```
Query Match      100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAACAAACACTGTCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAACAAACACTGTCTCTTTCTG 180

Qy 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTTGAACCAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTTGAACCAAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTTAAGGATCTCTTCAAGGCTCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTTAAGGATCTCTTCAAGGCTCTCAGCTAATT 300

Qy 301 CTTGGCTTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGTAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGTAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGACAAATGGCTGAGCATATAAAACATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480
Db 421 GGGACAAATGGCTGAGCATATAAAACATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480
```



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QY 481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
Db 481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
QY 541 GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAACAGATGATTGC 600
Db 541 GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAACAGATGATTGC 600
QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
Db 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647

RESULT 10
US-10-294-025-308
; Sequence 308, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-294-025-308

Query Match 100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 2,7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTTTCATTATCATGTAATCGGTCACTCAAGGGGCCAACACAGCTGGGGCCAC 60
Db 1 ACAGTTTCATTATCATGTAATCGGTCACTCAAGGGGCCAACACAGCTGGGGCCAC 60
QY 61 TGTCTAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATAA 120
Db 61 TGTCTAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATAA 120
QY 121 GNGCCTCAGATATAGATCTGTAGCAAGAAGAAGAAACAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCAGATATAGATCTGTAGCAAGAAGAAGAAACAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTCGACCTTTTGAACCTCTCTGACCCCTTTAGAACAGGCTACCTAATATCTG 240
Db 181 CCACCCCTCGACCTTTTGAACCTCTCTGACCCCTTTAGAACAGGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACACAGGCTCTCAAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACACAGGCTCTCAAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTAAGATGTGGTTCCACATTAGTTCTGATATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTAAGATGTGGTTCCACATTAGTTCTGATATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGTAATAAGTCAAGATGCCAGGGCCAGAGCAGGGGCTGCTCTTT 420
Db 361 CATTTTGTGTGTAATAAGTCAAGATGCCAGGGCCAGAGCAGGGGCTGCTCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAAACAAACAACATCAAGTCA 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAAACAAACAACATCAAGTCA 480
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QY 481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
Db 481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
QY 541 GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAACAGATGATTGC 600
Db 541 GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAACAGATGATTGC 600
QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
Db 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
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RESULT 11

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US-11-234-786-308
; Sequence 308, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-11-234-786-308
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Query Match 100.0%; Score 646; DB 16; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
DB 1 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
DB 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

QY 241 CTAGAGAAAAGAACCAACACCGCCCTCAAGAGATCTCTTACCAATGAAGTCTCAGCTAATT 300
DB 241 CTAGAGAAAAGAACCAACACCGCCCTCAAGAGATCTCTTACCAATGAAGTCTCAGCTAATT 300

QY 301 CTTGGCTAAGATCTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAAGATCTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
DB 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420

QY 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCAC 480
DB 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCAC 480

QY 481 TGTATCAATGGCATGAAGCTTGAGGACCTGAATCTACCGATTCTTTAAGGCAGCA 540
DB 481 TGTATCAATGGCATGAAGCTTGAGGACCTGAATCTACCGATTCTTTAAGGCAGCA 540

QY 541 GGACAGATTGAGTGCGCAACATGAGCAGCAGAGATCAATGGAACAAACAGATGATTC 600
DB 541 GGACAGATTGAGTGCGCAACATGAGCAGCAGAGATCAATGGAACAAACAGATGATTC 600

QY 601 AATGTCCTTTTTTCTCTGCTCTGCTGATGATAAAAGGGACCGT 647
DB 601 AATGTCCTTTTTTCTCTGCTCTGCTGATGATAAAAGGGACCGT 647

RESULT 12
US-10-294-025-1034
; Sequence 1034, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1034
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-1034

Query Match 93.0%; Score 600.8; DB 7; Length 2577;
Best Local Similarity 98.1%; Pred. No. 4.5e-186;
Matches 629; Conservative 0; Mismatches 8; Indels 4; Gaps 2;

QY 1 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
DB 636 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 695

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
DB 696 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 755

QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
DB 756 GGTGCTCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 815

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
DB 816 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 875

QY 241 CTAGAGAAAAGAACCAACACCGCCCTCAAGAGATCTCTTACCAATGAAGTCTCAGCTAATT 300
DB 876 CTAGAGAAAAGAACCAACACCGCCCTCAAGAGATCTCTTACCAATGAAGTCTCAGCTAATT 935

QY 301 CTTGGCTAAGATCTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB 936 CTTGGCTAAGATCTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 995

QY 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
DB 996 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 1054

QY 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCAC 480
DB 1055 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCAC 1111

QY 481 TGTATCAATGGCATGAAGCTTGAGGACCTGAATCTACCGATTCTTTAAGGCAGCA 540
DB 1112 TGTATCAATGGCATGAAGCTTGAGGACCTGAATCTACCGATTCTTTAAGGCAGCA 1171

QY 541 GGACAGATTGAGTGCGCAACATGAGCAGCAGAGATCAATGGAACAAACAGATGATTC 600
DB 1172 GGACAGATTGAGTGCGCAACATGAGCAGCAGAGATCAATGGAACAAACAGATGATTC 1231

QY 601 AATGTCCTTTTTTCTCTGCTCTGCTGATGATAAAAGGG 641
DB 1232 AATGTCCTTTTTTCTCTGCTCTGCTGATGATAAAAGGG 1272

RESULT 13
US-10-357-930-21476/c
; Sequence 21476, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281

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; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 21476
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A, T, C or G
US-10-357-930-21476

Query Match          92.8%; Score 599.2; DB 9; Length 1481;
Best Local Similarity 98.0%; Pred. No. 1.1e-185;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 60
Db 1097 ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 1038

QY 61 TGTCTCAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
Db 1037 TGTCTCAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 978

QY 121 GNGCCCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTTTCTG 180
Db 977 GGTGCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTTTCTG 918

QY 181 CCACCCCTCTGACCTTTGGAACCTCTGACCCCTTTAGAACAGGCTTACCTTAATATCTG 240
Db 917 CCACCCCTCTGACCTTTGGAACCTCTGACCCCTTTAGAACAGGCTTACCTTAATATCTG 858

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300
Db 857 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 798

QY 301 CTTGGCTTAAGATGTGGGTTCCCATTTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 797 CTTGGCTTAAGATGTGGGTTCCCATTTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 738

QY 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT 420
Db 737 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT 679

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACATCAAGTCTAC 480
Db 678 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACATCAAGTCTAC 622

QY 481 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 540
Db 621 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 562

QY 541 GGACCAAGTTTGAAGTGGCAACATGAGCAGAGAGATCAATGGAACAAACAGATGATTC 600
Db 561 GGACCAAGTTTGAAGTGGCAACATGAGCAGAGAGATCAATGGAACAAACAGATGATTC 502

QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 641
Db 501 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 461
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RESULT 14

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US-10-357-930-21536/c
; Sequence 21536, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; HUMAN PROSTATE CANCER
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; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21536
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A, T, C or G
US-10-357-930-21536
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Query Match          92.8%; Score 599.2; DB 9; Length 1481;
Best Local Similarity 98.0%; Pred. No. 1.1e-185;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 60
Db 1097 ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 1038

QY 61 TGTCTCAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
Db 1037 TGTCTCAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 978

QY 121 GNGCCCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTTTCTG 180
Db 977 GGTGCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTTTCTG 918

QY 181 CCACCCCTCTGACCTTTGGAACCTCTGACCCCTTTAGAACAGGCTTACCTTAATATCTG 240
Db 917 CCACCCCTCTGACCTTTGGAACCTCTGACCCCTTTAGAACAGGCTTACCTTAATATCTG 858

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300
Db 857 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 798

QY 301 CTTGGCTTAAGATGTGGGTTCCCATTTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 797 CTTGGCTTAAGATGTGGGTTCCCATTTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 738

QY 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT 420
Db 737 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT 679

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACATCAAGTCTAC 480
Db 678 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACATCAAGTCTAC 622

QY 481 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 540
Db 621 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 562

QY 541 GGACCAAGTTTGAAGTGGCAACATGAGCAGAGAGATCAATGGAACAAACAGATGATTC 600
Db 561 GGACCAAGTTTGAAGTGGCAACATGAGCAGAGAGATCAATGGAACAAACAGATGATTC 502
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03 ; Search time 222.451 Seconds
(without alignments)
6266.684 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattcatcatgta.....acttgataaaaggagccgt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	7	US-11-344-932-308 Sequence 308, App
2	599.2	92.8	2577	7	US-11-344-932-552 Sequence 552, App
3	58.6	9.1	201	6	US-10-284-444-1570 Sequence 1570, App
4	36.6	5.7	1566	9	US-11-174-307B-221 Sequence 221, App
5	36.6	5.7	1566	9	US-11-056-355B-75529 Sequence 75529, App
6	36	5.6	1145	6	US-10-953-349-1766 Sequence 1766, App
7	35.4	5.5	715	8	US-11-266-748A-407591 Sequence 407591, App
8	35.4	5.5	715	8	US-11-266-748A-478637 Sequence 478637, App
9	34.8	5.4	74930	7	US-11-454-296-1 Sequence 1, Appli
10	34.6	5.4	943	8	US-11-266-748A-214211 Sequence 214211, App
11	34.6	5.4	945	8	US-11-266-748A-76796 Sequence 76796, App
12	34.6	5.4	945	8	US-11-266-748A-129607 Sequence 129607, App
13	34.4	5.3	87977	10	US-11-330-726-145 Sequence 145, App
14	33.8	5.2	2704	9	US-11-056-355B-46304 Sequence 46304, App
15	33.4	5.2	633	7	US-11-454-296-35 Sequence 35, Appl
16	33.4	5.2	142281	8	US-11-266-748A-213957 Sequence 213957, App
17	33	5.1	572	8	US-11-266-748A-215548 Sequence 215548, App
18	32.6	5.0	1472	6	US-10-449-902-19300 Sequence 19300, App
19	32.6	5.0	1472	6	US-10-449-902-19357 Sequence 19357, App
20	32.6	5.0	3538	6	US-10-449-902-25041 Sequence 25041, App
21	32.4	5.0	1308	9	US-11-293-582-14 Sequence 14, Appl
22	32.4	5.0	119057	6	US-10-539-228-609 Sequence 609, App

23	32.4	5.0	254396	6	US-10-540-898-534 Sequence 534, App
24	32.4	5.0	816609	10	US-11-073-360-1606 Sequence 1606, App
25	32.2	5.0	663	7	US-11-371-354-10070 Sequence 10070, App
26	32.2	5.0	663	7	US-11-371-354-75580 Sequence 75580, App
27	32.2	5.0	2907	6	US-10-612-783-1529 Sequence 1529, App
28	32.2	5.0	3031	9	US-11-218-305-1072 Sequence 1072, App
29	32.2	5.0	189056	8	US-11-266-748A-100812 Sequence 100812, App
30	32	5.0	521	8	US-11-266-748A-153623 Sequence 153623, App
31	32	5.0	521	8	US-11-338-399-9 Sequence 9, Appli
32	32	5.0	1611	8	US-11-174-307B-2477 Sequence 2477, App
33	32	5.0	1855	9	US-11-056-355B-101312 Sequence 101312, App
34	32	5.0	1855	9	US-11-056-355B-112551 Sequence 112551, App
35	32	5.0	1856	9	US-11-174-307B-321 Sequence 321, App
36	32	5.0	1856	9	US-11-056-355B-37911 Sequence 37911, App
37	32	5.0	3021	6	US-10-449-902-25119 Sequence 25119, App
38	32	5.0	3667	6	US-10-449-902-23178 Sequence 23178, App
39	32	5.0	794	8	US-11-266-748A-39970 Sequence 39970, App
40	31.6	4.9	794	8	US-11-266-748A-214583 Sequence 214583, App
41	31.6	4.9	794	8	US-11-266-748A-237140 Sequence 237140, App
42	31.6	4.9	3883	6	US-10-449-902-18938 Sequence 18938, App
43	31.6	4.9	73634	10	US-11-330-726-121 Sequence 121, App
44	31.6	4.9	811284	6	US-10-833-833-128 Sequence 128, App
45	31.6	4.9	811284	6	US-10-833-833-128 Sequence 128, App

ALIGNMENTS

RESULT 1

US-11-344-932-308
; Sequence 308, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-308

Query Match      100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 9.9e-205; Mismatches 0; Indels 0; Gaps 0;
Matches 647; Conservative 0;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATCGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACTGATCTCTTCTG 180
Db 121 GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACTGATCTCTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAAGCAACCAACGGCCTCAAGAGATCTCTTACATGAGGTCTCAGCTAATT 300
Db 241 CTAGAGAAAAGCAACCAACGGCCTCAAGAGATCTCTTACATGAGGTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGAGAGGGGGCTGCTTGTCTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGAGAGGGGGCTGCTTGTCTT 420

Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAAACATCAAGTCTAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAAACATCAAGTCTAC 480

Qy 481 TGTATCAATTCGATGAAGACTTGGAGGACCTGAATCTACCGATTTCATCTTAAGGCACA 540
Db 481 TGTATCAATTCGATGAAGACTTGGAGGACCTGAATCTACCGATTTCATCTTAAGGCACA 540

Qy 541 GGACAGGTTTGTAGTGGCAACAATGACAGCAGAGATCAATGGAACAAACAGAAATGATTC 600
Db 541 GGACAGGTTTGTAGTGGCAACAATGACAGCAGAGATCAATGGAACAAACAGAAATGATTC 600

Qy 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
Db 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
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US-11-344-932-552
; Sequence 552, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 552
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-552

Query Match      92.8%; Score 599.2; DB 7; Length 2577;
Best Local Similarity 98.0%; Pred. No. 8.8e-189;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACCTCAAGGGGCCCAACACAGCTGGAGCCAC 60
Db 636 ACGATTTTCATTATCATGTAATCGGTCACCTCAAGGGGCCCAACACAGCTGGAGCCAC 695

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 75529
; LENGTH: 1566
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ceres Seq. ID no. 6443376
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 15175923
; OTHER INFORMATION: as cited in SEQ ID NO 54037
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13503610
; OTHER INFORMATION: as cited in SEQ ID NO 62416
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13657610
; OTHER INFORMATION: as cited in SEQ ID NO 66165
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13598312
; OTHER INFORMATION: as cited in SEQ ID NO 68448
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1566)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13596100
; OTHER INFORMATION: as cited in SEQ ID NO 68573
US-11-056-355B-75529

Query Match      5.7%; Score 36.6; DB 9; Length 1566;
Best Local Similarity 53.1%; Pred. No. 0.31;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 371 GTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGGGGGCTGCTTTGGGAACAATG 430
Db 1372 GAGGCTAAAGTAGGATGAAGAAAGAAACCGGGTTTGGCAGATTGCTTTGGAAAGTGG 1431
Qy 431 GCTGAGCATATAACCATAGGTTATGGGGAACAAACAAACATCAAAAGTCACCTGTATCAATT 490
Db 1432 TTTAAGTGTAAACAGTGCAGTTTGGGTGGCTCTTAAACAATGTCAAGCCCTTCGGTTAGTATC 1491
Qy 491 GCCATGAAGACTTGAGGACCTGAATC 517
Db 1492 COTGGGAACACTGCATCGACCGATATC 1518

RESULT 6
US-10-953-349-1766/c
; Sequence 1766, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1766
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1766
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Query Match      5.6%; Score 36; DB 6; Length 1145;
Best Local Similarity 48.5%; Pred. No. 0.41;
Matches 99; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 400 GAGCAGGGGCTGCTTGGGAAACAATGGCTGAGCATATTAACCATAGTTATGGGA 459
Db 900 GACCAAGAGGCCACATATGAGAATCACAGCGTATAAGCTAAATCCATAAGAAGTGCATC 841
Qy 460 ACAAACAACATCAAGTCACTGTATCAATTCCTCAAGACCTTGAGGGACCTGAATCTA 519
Db 840 CATTATCTTCACCATCATCACCGTCTCCNAAGCGTTGCCCTACTTGGTCCCAATACCCGTG 781
Qy 520 CCGATTTCATCTTAAGGCAGCAGGACCACTTTGAGTGGCAACAATGCAGCAGCAATCAA 579
Db 780 CCGCTCGTCAACGCTCCCTGAGCGCCGAGGAGAGTCTCCAGCATGACTCAGCAGAACAG 721
Qy 580 TGGAAACAACACAGAATGATTGCAAT 603
Db 720 TCCAAGCACAATTTGTGGCATCAGT 697

RESULT 7
US-11-266-748A-407591/c
; Sequence 407591, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 407591
; LENGTH: 715
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-407591
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Query Match      5.5%; Score 35.4; DB 8; Length 715;
Best Local Similarity 66.2%; Pred. No. 0.5;
Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 28 TCATCTAAGGGGCCAACCAACAGCTGGGAGCCACTGCTCAGGGGAGGTTTCATATGGGACT 87
Db 317 TGATTCCAGTGGGAGCCAGGTTTGGGAACCACTTCTATGGGATGGTCCATCTGGGAAT 258
Qy 88 TTCTACTGCCCAAGGTT 104
Db 257 TGGCTGTCCACAGGTT 241

RESULT 8
US-11-266-748A-478637
```


; Sequence 478637, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 478637
; LENGTH: 715
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-478637

Query Match 5.5%; Score 35.4; DB 8; Length 715;
Best Local Similarity 66.2%; Pred. No. 0.5;
Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 28 TCACCTACGGGGCAACACAGCTGGAGCCATGTCAGGGGAAGTTTCATATGGGACT 87
DB 399 TGATCCAGTGGGCGCCAGCTTGGGAACCACTTCTATGGGGATGGTCCATCTGGGAAT 458
QY 88 TTCTACTGCCCAAGGTT 104
DB 459 TGGCTGTCCACAGGTT 475

RESULT 9
US-11-454-296-1/c
; Sequence 1, Application US/11454296
; Publication No. US20060286588A1
; GENERAL INFORMATION:
; APPLICANT: SAINZ, Jesus
; APPLICANT: GRANT, Struan F. A.
; TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR
; TITLE OF INVENTION: RISK OF TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: 2345.2069-002
; CURRENT APPLICATION NUMBER: US/11/454,296
; CURRENT FILING DATE: 2006-06-16
; PRIOR APPLICATION NUMBER: US 60/692,174
; PRIOR FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US 60/757,155
; PRIOR FILING DATE: 2006-01-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 74930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-454-296-1

Query Match 5.4%; Score 34.8; DB 7; Length 74930;

Best Local Similarity 51.7%; Pred. No. 11;
Matches 78; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 12 TATCATGTAATCGGTCTCACTCAAGGGCCACACAGCTGGAGCCACTGCTTCAGGGGA 71
DB 50371 TAACATTAAAGACAGTTTCACTCAGGAACCAACAGAACTTAGACACAATGCTTTAAGC 50312
QY 72 AGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAAGGNGGCCTCACA 131
DB 50311 ACATGGAGAGAGCCCTTTATGCTTCTCAAGGCCAACTCTACTTAATCATCAGTTAATGAAT 50252
QY 132 GTATAGATCTGTAGCAAGAAAGAAACA 162
DB 50251 GCTTGGAGGGATATAAGATATAAGGAGACA 50221

RESULT 10
US-11-266-748A-214211/c
; Sequence 214211, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 214211
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (869)..(869)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-214211

Query Match 5.4%; Score 34.6; DB 8; Length 943;
Best Local Similarity 53.3%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 347 AGGGTCAATTTGCTCTATTTGTGTGGATAAAGTCAGGATCCAGGGGGCCAGAGCAGG 406
DB 657 AGGGTAATAAAGTGGGCTTCTTAGGTCGAGAAATTCGGGTCTACTCGGGCTACTTTTCG 598
QY 407 GGGCTGCTTGTGTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAACAAAAC 466
DB 597 GAATCTTTAGTGTGGTCTTAGGSCACTGCACTCTCACACCAGCTGATGGGAACCATCTG 538
QY 467 AACATCAAGTCACTGT 483
DB 537 GATACCTGACTCACTGT 521

RESULT 11
US-11-266-748A-76796/c
; Sequence 76796, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76796
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-76796

Query Match 5.4%; Score 34.6; DB 8; Length 945;
Best Local Similarity 53.3%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 347 AGGTCATTTGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGG 406
Db 683 AGGGTAAAGTGGCTTCTTAGTCTGCAAGAAATTCGGGTTGTACTCGGGCTACTTTCCG 624

Qy 407 GGGCTGCTTGTCTTGGGACAAATGCTGAGCATATAACCATAGGTTATGGGGAACAAAC 466
Db 623 GAATTCCTTAGTGTGGGCTTAGGGCACTGCATCTCACACGCTGATGGGAACCATCTG 564

Qy 467 AACATCAAAGTCACGT 483
Db 563 GATACCTGACTCACTGT 547

RESULT 12
US-11-266-748A-129607
; Sequence 129607, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129607
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-129607

Query Match 5.4%; Score 34.6; DB 8; Length 945;
Best Local Similarity 53.3%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 347 AGGTCATTTGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGG 406
Db 263 AGGGTAAAGTGGCTTCTTAGTCTGCAAGAAATTCGGGTTGTACTCGGGCTACTTTCCG 322

Qy 407 GGGCTGCTTGTCTTGGGACAAATGCTGAGCATATAACCATAGGTTATGGGGAACAAAC 466
Db 323 GAATTCCTTAGTGTGGGCTTAGGGCACTGCATCTCACACGCTGATGGGAACCATCTG 382

Qy 467 AACATCAAAGTCACGT 483
Db 383 GATACCTGACTCACTGT 399

RESULT 13
US-11-330-726-145
; Sequence 145, Application US/11330726
; Publication No. US20060204982A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 20366-011002
; CURRENT APPLICATION NUMBER: US/11/330,726
; CURRENT FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 87977
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2001)..(2048)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6720)..(7498)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8834)..(8882)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: (16167)..(16186)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24443)..(24580)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28778)..(28871)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45952)..(46750)
; OTHER INFORMATION: n = a, c, g, or t
US-11-330-726-145

Query Match          5.3%; Score 34.4; DB 10; Length 87977;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 71; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 316 GGTTCACATAGTTCTCAATATGGGGGAAGGGTCAATTTGCTCATTTTGTGTGGA 375.
Db 70644 GGTGTCCTCATAGTCTCTGACTATAACAGTACTGTGTGATGGGCCAAACTGGGAGCA 70703

QY 376 TAAAGTCAGGATGCCCGAGGGCCAGACGAGGGGGCTGTGCTTTGGGAACAATGGCTGA 435
Db 70704 TCATCTCATTTGGAATCACAGAGAAGCAGGGGTATGCTCCCAATGGGAGCAGAGCTGA 70763

QY 436 GCATATAACCAT 447
Db 70764 GCACATAAAGAT 70775

RESULT 14
US-11-056-355B-46304/c
; Sequence 46304, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46304
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2704)
; OTHER INFORMATION: Ceres Seq. ID no. 13578529
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2704)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13582297
; OTHER INFORMATION: as cited in SEQ ID NO 56486
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2704)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13586936
; OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-46304

Query Match          5.2%; Score 33.8; DB 9; Length 2704;
Best Local Similarity 52.5%; Pred. No. 3.6;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 463 AAACACATCAAGTCATCTATCAATGCCATGAAGACTTGAGGGACCTGAATCTACCG 522
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Db 753 ACACAAACAAGAACATCAACAGGACGATTTCATGAGCATCAGGGATATTAGGATCTGCTC 694
QY 523 ATTCACTTTAAGGACGAGGACCACTTTGAGTGGCAACAATGCCAGCAGCAATCAATGG 582
Db 693 CTACACTCAAAGCAACTTGGACAACATCCAAGGAATTCACAGAAGCACCAGAAGCAGCGC 634
QY 583 AAACAAACAGAATGATTGCAAT 603
Db 633 AATGAAGACGACTACTTTTAT 613

RESULT 15
US-11-454-296-35/c
; Sequence 35, Application US/11454296
; Publication No. US20060286588A1
; GENERAL INFORMATION:
; APPLICANT: GRANT, Struan P. A.
; APPLICANT: SAINZ, Jesus
; TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR
; TITLE OF INVENTION: RISK OF TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: 2345.2069-002
; CURRENT APPLICATION NUMBER: US/11/454,296
; CURRENT FILING DATE: 2006-06-16
; PRIOR APPLICATION NUMBER: US 60/692,174
; PRIOR FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US 60/757,155
; PRIOR FILING DATE: 2006-01-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-454-296-35

Query Match          5.2%; Score 33.4; DB 7; Length 633;
Best Local Similarity 60.4%; Pred. No. 2.2;
Matches 55; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 12 TATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCACTGCTCAGGGGA 71
Db 141 TAACATTAAAGACAGTTTTCACCTCAGGAAACCAACAGAACTTAGACACAATGCTTAGAAGC 82
QY 72 AGGTTCAATCGGACTTTTCTACTGCCCAAGG 102
Db 81 ACATGGAGACGAGCCTTTATGCTTCTCAAGG 51

Search completed: December 31, 2006, 19:49:07
Job time : 225.451 secs
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GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: December 31, 2006; 12:07:59 ; Search time 502.906 Seconds
(without alignments)
8969.963 Million cell updates/sec
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Perfect score: 646
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Gapop 10.0 , Gapext 1.0
Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s : *
3: Geneseqn2000s : *
4: Geneseqn2001as : *
5: Geneseqn2001bs : *
6: Geneseqn2002as : *
7: Geneseqn2002bs : *
8: Geneseqn2003as : *
9: Geneseqn2003bs : *
10: Geneseqn2003cs : *
11: Geneseqn2003ds : *
12: Geneseqn2004as : *
13: Geneseqn2004bs : *
14: Geneseqn2005as : *
15: Geneseqn2006s : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	3	Aaa06540 Human imm
2	646	100.0	647	4	Aah93656 Human pro
3	646	100.0	647	4	Aas63749 Human pro
4	646	100.0	647	4	Aah02721 Prostate
5	646	100.0	647	4	Aah84970 Human pro
6	646	100.0	647	4	Aaf86940 Human P71
7	646	100.0	647	5	Acc59557 Prostate
8	646	100.0	647	6	Ab195120 Human P71
9	646	100.0	647	8	Acc95284 Prostate
10	646	100.0	647	10	Adb13758 Human pro
11	646	100.0	647	10	Adg26174 Human pro
12	646	100.0	647	15	Aef66455 Human pro
13	600.8	93.0	2577	10	Adb14484 Human pro
C 14	599.2	92.8	1481	5	Abv21571 Human pro
C 15	599.2	92.8	1481	5	Abv21485 Human pro
C 16	599.2	92.8	1481	5	Abv27938 Human pro
C 17	599.2	92.8	1481	5	Abv21587 Human pro
C 18	599.2	92.8	1481	5	Abv21545 Human pro

C 19	599.2	92.8	1481	5	ABV27364	Human pro
C 20	599.2	92.8	1481	5	ABV27390	Human pro
C 21	599.2	92.8	1481	5	ABV22098	Human pro
C 22	599.2	92.8	1481	5	ABV25790	Human pro
C 23	599.2	92.8	2577	4	Aah93830	Human pro
24	599.2	92.8	2577	4	AAS63923	Human pro
25	599.2	92.8	2577	5	ACA59731	Prostate
26	599.2	92.8	2577	6	ABL95294	Human P71
27	599.2	92.8	2577	8	ACC95458	Prostate
28	599.2	92.8	2577	10	ADB14002	Human pro
29	599.2	92.8	2577	10	ADG26418	Human pro
30	599.2	92.8	2577	15	Aef66699	Human pro
31	597.6	92.5	1454	6	AAD38826	Human PSN
32	401.6	62.2	452	14	ACL55651	Human col
33	357.6	55.4	815	5	ABV11648	Human pro
34	265.8	41.1	790	5	ABV11499	Human pro
35	260	40.2	671	5	ABV41718	Human pro
36	260	40.2	671	5	ABV41569	Human pro
37	260	40.2	671	5	ABV38602	Human pro
C 38	256.4	39.7	608	5	ABV27406	Human pro
C 39	256.4	39.7	608	5	ABV27303	Human pro
C 40	256.4	39.7	608	5	ABV25591	Human pro
41	250	38.7	616	5	ABV32793	Human pro
42	229	35.4	554	14	ACL55144	Human col
43	217.4	33.7	690	5	ABV02479	Human pro
44	214.6	33.2	543	5	ABV08703	Human pro
45	199	30.8	294	3	Aaz95017	Prostate

ALIGNMENTS

RESULT 1
Aaa06540
ID Aaa06540 standard; cDNA; 647 BP.
XX
AC Aaa06540;
XX
13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:308.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
PS Claim 1; Page 198; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an

CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
CC the present invention

XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60
DB |||||||
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60
DB |||||||

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATATA 120
DB |||||||

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATATA 120
DB |||||||

QY 121 GGGCCCTCACAGTATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
DB |||||||

QY 121 GGGCCCTCACAGTATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
DB |||||||

QY 181 CCACCCCTTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
DB |||||||

QY 181 CCACCCCTTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
DB |||||||

QY 241 CTAGAGAAAGACCAACACCGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300
DB |||||||

QY 241 CTAGAGAAAGACCAACACCGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300
DB |||||||

QY 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360
DB |||||||

QY 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360
DB |||||||

QY 361 CATTGTTGTGTGGATAAAGTCAGATGCCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
DB |||||||

QY 361 CATTGTTGTGTGGATAAAGTCAGATGCCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
DB |||||||

QY 421 GGGACAATGGCTGAGCATATAACCATAGGTTATGSGGAACAAACAAACATCAAGTCAC 480
DB |||||||

QY 421 GGGACAATGGCTGAGCATATAACCATAGGTTATGSGGAACAAACAAACATCAAGTCAC 480
DB |||||||

QY 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAAATCTACCGATTTCATCTTAAAGCAGCA 540
DB |||||||

QY 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAAATCTACCGATTTCATCTTAAAGCAGCA 540
DB |||||||

QY 541 GGAACAGTTTGTAGTGGCAACAATCAGCAGCAGGAATCAATGGAACAACAGATGATTC 600
DB |||||||

QY 541 GGAACAGTTTGTAGTGGCAACAATCAGCAGCAGGAATCAATGGAACAACAGATGATTC 600
DB |||||||

QY 601 AATGTCCTTTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
DB |||||||

QY 601 AATGTCCTTTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
DB |||||||

RESULT 2

AAH93656

ID AAH93656 standard; cDNA; 647 BP.

XX

AAH93656;

AC

DT 04-OCT-2001 (first entry)

XX

DE Human prostate-specific cDNA sequence P712P.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cystostatic; gene therapy; metastasis; ss.

OS Homo sapiens.

PN WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
XX vaccines.

XX Claim 1; Page 324; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention

XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 4; Length 647;

Best Local Similarity 100.0%; Pred. No. 6.6e-200;

Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60

DB |||||||

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATATA 120

DB |||||||

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTATACAGGATATATA 120

DB |||||||

QY 121 GGGCCCTCACAGTATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180

DB |||||||

QY 121 GGGCCCTCACAGTATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180

DB |||||||

QY 181 CCACCCCTTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

DB |||||||

QY 241 CTAGAGAAAGACCAACAAACCGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300

DB |||||||

QY 241 CTAGAGAAAGACCAACAAACCGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300

DB |||||||

QY 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360

DB |||||||

QY 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360

DB |||||||


```
XX 12-APR-2001.
XX
XX
XX 04-OCT-2000; 2000WO-US027464.
XX
XX 04-OCT-1999; 99US-0157455P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX WPI; 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX
XX Claim 4; Page 210; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising at
XX least an immunogenic portion of a prostate tumour antigen protein or its
XX variant. (I) have cytostatic activity and can be used in vaccine
XX production. (I), prostate tumour antigen polynucleotides, an antigen
XX presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
XX pharmaceutical composition containing (I) are useful for inhibiting the
XX development of cancer in a patient. Antibodies specific for prostate
XX specific proteins and oligonucleotides that hybridise to a polynucleotide
XX that encodes a prostate specific protein are useful for detecting the
XX presence or absence of a cancer or monitoring the progression the
XX progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
XX AAH74798 to AAH74821 and AAH74830 are sequences used in the
XX exemplification of the present invention
XX
XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 646; DB 4; Length 647;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-200;
XX Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GNGGCTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTTTCTG 180
DB 121 GNGGCTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 240
QY 241 CTAGAGAAAGAACCAACAGCCCTCAAGAGTCTCTTACCATGAAGGTCTCAGCTAAT 300
DB 241 CTAGAGAAAGAACCAACAGCCCTCAAGAGTCTCTTACCATGAAGGTCTCAGCTAAT 300
QY 301 CTTGGCTAAGATGTGGGTTTCCACATTAGTCTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
DB 301 CTTGGCTAAGATGTGGGTTTCCACATTAGTCTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTTGCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTTGCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATTAACATAGGTTATGGGGAAACAAACATCAAGAGTCAC 480
DB 421 GGGAAACAATGGCTGAGCATATTAACATAGGTTATGGGGAAACAAACATCAAGAGTCAC 480
QY 481 TGATATCAATTGCGATGAAGACTTTGAGGACCTGAACTCTACCGATTTCATCTTAAGGCAGCA 540
DB 481 TGATATCAATTGCGATGAAGACTTTGAGGACCTGAACTCTACCGATTTCATCTTAAGGCAGCA 540
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QY 541 GGACCACTTTGAGTGGCAACAATCCACAGCAGAGTCAATGGAACCAACAGATGATTGC 600
DB 541 GGACCACTTTGAGTGGCAACAATGCGACAGCAGAGTCAATGGAACCAACAGATGATTGC 600
QY 601 AATGTCCTCTTTTCTCTGCTTCTGACTTTGATATAAAGGGGACCGT 647
DB 601 AATGTCCTCTTTTCTCTGCTTCTGACTTTGATATAAAGGGGACCGT 647
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RESULT 5

AAH84970
ID AAH84970 standard; cDNA; 647 BP.

XX AAH84970;

DT 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence P712P.

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.

XX Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030904.

XX 12-NOV-1999; 99US-00439313.

XX 18-NOV-1999; 99US-00443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;

XX WPI; 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a
XX prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer.

XX Claim 5; Page 224; 325pp; English.

XX The present invention describes an isolated polypeptide (P1) comprising
XX at least an immunogenic portion of a prostate-specific protein, or its
XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX (N1) have cytostatic activity and can be used in vaccine production. The
XX polypeptides, nucleic acids and antibodies from the present invention are
XX useful in the diagnosis and therapy of prostate cancer. Prostate specific
XX genes P704P, P712P, P774P, P775P and B305D are located in a genomic
XX region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
XX Prostate specific antigen (PSA) P501S was located on chromosome 1.
XX AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
XX and polypeptide sequences used in the exemplification of the present
XX invention

XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 646; DB 4; Length 647;

XX Best Local Similarity 100.0%; Pred. No. 6.6e-200;

XX Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 60

DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCGCCAAAGGTTCTATACAGGATATAA 120
QY 121 GGGGCTTCAGATATAGATCTGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GGGGCTTCAGATATAGATCTGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTTCGACCCCTTTGGAATCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
Db 181 CCACCCCTTCGACCCCTTTGGAATCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTTACCATGAGGTTCTAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTTACCATGAGGTTCTAGCTAAT 300
QY 301 CTTGGCTTAAGATGTGGTTCCACATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTTAAGATGTGGTTCCACATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAAGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGGAAACATGGCTGAGCATATACCATAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
Db 421 GGGAAACATGGCTGAGCATATACCATAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
QY 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
Db 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
QY 541 GGAACAGTTTGTAGTGGCAACAATGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
Db 541 GGAACAGTTTGTAGTGGCAACAATGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
QY 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGGACCGT 647

RESULT 6
AAF86940
ID AAF86940 standard; cDNA; 647 BP.
XX
AC AAF86940;
XX
DT 06-JUL-2001 (first entry)
XX
DE Human P712P inventive antigen coding sequence SEQ ID NO: 335.
XX
DE Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor; ss.
XX
OS Homo sapiens.
XX
PN WO200125273-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US027465.
XX
PR 04-OCT-1999; 99US-0157459P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX WPI; 2001-328324/34.
XX
PT Polypeptide comprising part of the Wilm's Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WTI.
XX
PS Disclosure; Page 214; 228pp; English.

XX The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a coding sequence used in the exemplification of the invention
XX
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
Query Match 100.0%; Score 646; DB 4; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCATTTTCATTATCATATGTAATCGGTCACCTCAGGGGCCAACCCAGCTGGAGCCAC 60
Db 1 AGCATTTTCATTATCATATGTAATCGGTCACCTCAGGGGCCAACCCAGCTGGAGCCAC 60
QY 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCAAGGTTCTATACAGATATAA 120
Db 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCAAGGTTCTATACAGATATAA 120
QY 121 GGGGCTTCAGATATAGATCTGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GGGGCTTCAGATATAGATCTGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTTCGACCCCTTTGGAATCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
Db 181 CCACCCCTTCGACCCCTTTGGAATCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTTACCATGAGGTTCTAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTTACCATGAGGTTCTAGCTAAT 300
QY 301 CTTGGCTTAAGATGTGGTTCCACATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTTAAGATGTGGTTCCACATTAAGTTCTGAAATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAAGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGGAAACATGGCTGAGCATATACCATAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
Db 421 GGGAAACATGGCTGAGCATATACCATAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
QY 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
Db 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
QY 541 GGAACAGTTTGTAGTGGCAACAATGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
Db 541 GGAACAGTTTGTAGTGGCAACAATGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
QY 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGGACCGT 647

RESULT 7
ACA59557
ID ACA59557 standard; cDNA; 647 BP.
XX
AC ACA59557;
XX
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #300.
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;

KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
XX 29-JUN-2001; 2001US-00895793.
XX PF
XX 04-OCT-1999; 99US-0157455P.
PR
PR 04-OCT-2000; 2000US-00679272.
PR
PR 28-MAR-2001; 2001US-00822827.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T W.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR WPI; 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
PT
XX
XX Example 3; SEQ ID NO 308; 85pp; English.
PS
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 5; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATATCATGTAATTCGGGTCACTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60
DB 1 ACGATTTTCATATCATGTAATTCGGGTCACTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GNGCCCTCACAGTATAGATCTGGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180
DB 121 GNGCCCTCACAGTATAGATCTGGTAGCAAGAAGAGAGAAACAAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTTGACCCCTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTATATCTG 240
DB 181 CCACCCCTTGACCCCTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTATATCTG 240
QY 241 CTAGAGAAAAGACCAACCAAGCGCTCAAGAGATCTCTTACCATCAAGGTCTCAGCTAATT 300
DB 241 CTAGAGAAAAGACCAACCAAGCGCTCAAGAGATCTCTTACCATCAAGGTCTCAGCTAATT 300
QY 301 CTTGGCTAAGATGTGGGTTCACATATTAGGTTCTGAATATGCGGGGAAGGGTCAATTGGCT 360
DB 301 CTTGGCTAAGATGTGGGTTCACATATTAGGTTCTGAATATGCGGGGAAGGGTCAATTGGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTTT 420
QY 421 GGGNACAATGGCTGAGCATATTAACCATAGGTTTATGGGGAAACAAACACATCAAGTCAC 480
DB 421 GGGNACAATGGCTGAGCATATTAACCATAGGTTTATGGGGAAACAAACACATCAAGTCAC 480
QY 481 TGTATCAATTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATTTAAGGCAGCA 540
DB 481 TGTATCAATTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATTTAAGGCAGCA 540
QY 541 GGACCACTTTGAGTGGCAACAATGTCAGCAGCAGCAATCAATGCGAAAACACAGATGATTGC 600
DB 541 GGACCACTTTGAGTGGCAACAATGTCAGCAGCAGCAATCAATGCGAAAACACAGATGATTGC 600
QY 601 AATGTCCTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
DB 601 AATGTCCTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647

RESULT 8
ABL95120
ID ABL95120 standard; cDNA; 647 BP.
XX
AC ABL95120;
XX
XX 19-JUL-2002 (first entry)
DT
XX Human P712P cDNA sequence SEQ ID NO 308.
DE
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX US2002022248-A1.
PN
XX 21-FEB-2002.
PD
XX 12-JAN-2001; 2001US-00759143.
PF
XX 25-FEB-1997; 97US-00806099.
PR
XX 01-AUG-1997; 97US-00904804.
PR
XX 10-FEB-1998; 98US-00020956.
PR
XX 25-FEB-1998; 98US-00030607.
PR
XX 14-JUL-1998; 98US-00115453.
PR
XX 23-SEP-1998; 98US-00159812.
PR
XX 09-APR-1999; 99US-00288946.
PR
XX 13-JUL-1999; 99US-00352616.
PR
XX 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 10-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 XX
 (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIANG/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDWICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI; 2002-255649/30.
 DR
 XX
 XX New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 PS Claim 1; SEQ ID NO 308; 87pp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention
 XX
 SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
 Query Match 100.0%; Score 646; DB 6; Length 647;
 Best Local Similarity 100.0%; Pred. No. 6.6e-200; Mismatches 0; Gaps 0;
 Matches 647; Conservative 0; Indels 0; Gaps 0;
 QY 1 ACAGTTTTCATTATCATGTAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
 DB 1 ACAGTTTTCATTATCATGTAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
 QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
 DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
 QY 121 GGGCCCTCAGATATAGATCTGTAGCAAGAGAGAGAAACAACTGATCTCTTCTG 180
 DB 121 GGGCCCTCAGATATAGATCTGTAGCAAGAGAGAGAAACAACTGATCTCTTCTG 180
 QY 181 CCACCCCTCGACCTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
 DB 181 CCACCCCTCGACCTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
 QY 241 CTAGAGAAAGACCAACAGGGCTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300
 DB 241 CTAGAGAAAGACCAACAGGGCTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300

QY 301 CTTGGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTTCAATTGCT 360
 DB 301 CTTGGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTTCAATTGCT 360
 QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTCTTT 420
 DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTCTTT 420
 QY 421 GGGAAACAATGGCTGAGCATATACCATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480
 DB 421 GGGAAACAATGGCTGAGCATATACCATAGTTTATGGGAAACAAACAAACATCAAGTCTAC 480
 QY 481 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
 DB 481 TGTATCAATTGGCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
 QY 541 GGACCAAGTTTGAAGTGCAACAATGAGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
 DB 541 GGACCAAGTTTGAAGTGCAACAATGAGCAGCAGCAGATCAATGGAACAACAGATGATTC 600
 QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
 DB 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647

RESULT 9

ACC95284
 ID ACC95284 standard; cDNA; 647 BP.

XX ACC95284;

XX 28-AUG-2003 (first entry)

XX Prostate tumour specific cDNA sequence SEQ ID 308.

XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;

XX Immune response; prostate cancer; ss.

XX Homo sapiens.

XX WO200289747-A2.

XX 14-NOV-2002.

XX 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

XX 29-JUN-2001; 2001US-00895814.

XX 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;

XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;

XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;

XX McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;

XX Deng T;

XX WPI; 2003-167130/16.

XX New prostate-specific proteins and genes, useful in gene therapy.

XX Particularly for stimulating an immune response in a patient, or treating

XX prostate cancer in a patient, as well as for diagnosing prostate cancer

XX in a patient.

XX Example 3; Page 391-392; 691pp; English.

XX The present invention relates to novel prostate-specific proteins (PSP)

XX and their coding sequences. The PSPs and their coding sequences are

XX useful for stimulating an immune response in a patient, or for treating

XX prostate cancer in a patient and for determining, detecting or diagnosing

XX the presence of a cancer in a patient. The present sequence was used to

CC	illustrate the invention	
XX		
SQ	Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;	
	Query Match	
	Best Local Similarity 100.0%; Score 646; DB 8; Length 647;	
	Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ACGATTTTCATATCATGTAATCGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60	
Db		
1	ACGATTTTCATATCATGTAATCGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60	
61	TGCTCAGGGGAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120	
Db		
61	TGCTCAGGGGAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120	
121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACCTGATCTCTTCTG 180	
Db		
121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACCTGATCTCTTCTG 180	
181	CCACCCCTTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240	
Db		
181	CCACCCCTTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240	
241	CTAGAGAAAGACCAACACCGCCTCAAGGATCTTTACCATGAAGTCTCAGCTAATT 300	
Db		
241	CTAGAGAAAGACCAACACCGCCTCAAGGATCTTTACCATGAAGTCTCAGCTAATT 300	
301	CTTGCTTAAGATGTGGGTTCCACATTTAGTTCTGTAATATGGGGGAAGGGTCAATTTGCT 360	
Db		
301	CTTGCTTAAGATGTGGGTTCCACATTTAGTTCTGTAATATGGGGGAAGGGTCAATTTGCT 360	
361	CATTTTGTGTGTAAGTAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420	
Db		
361	CATTTTGTGTGTAAGTAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420	
421	GGGAACAATGGCTGAGCATATTAACATAGTTATGGGGAACAAACACATCAAGTCTAC 480	
Db		
421	GGGAACAATGGCTGAGCATATTAACATAGTTATGGGGAACAAACACATCAAGTCTAC 480	
481	TGTATCAATTGTCATGAAGCTTTGAGGACCTGAATCTACCATTTCACTTTAAGGCAGCA 540	
Db		
481	TGTATCAATTGTCATGAAGCTTTGAGGACCTGAATCTACCATTTCACTTTAAGGCAGCA 540	
541	GGACAGTTTGATGGCAACAATGCAGCAGCAGAGATCAATGGAACAAACAGAAATGATGC 600	
Db		
541	GGACAGTTTGATGGCAACAATGCAGCAGCAGAGATCAATGGAACAAACAGAAATGATGC 600	
601	AATGTCCTTTTCTCTGCTTCTGACTTGATTAAGGGGACCGT 647	
Db		
601	AATGTCCTTTTCTCTGCTTCTGACTTGATTAAGGGGACCGT 647	
	RESULT 10	
ADBI3758		
ID	ADBI3758 standard; cDNA; 647 BP.	
AC	ADBI3758;	
XX		
DT	18-DEC-2003 (first entry)	
XX		
DE	Human prostate specific cDNA P7112P.	
XX		
KW	Human; ss; prostate specific cDNA; cytostatic; immunostimulant;	
KW	Gene therapy; cell therapy; vaccine; T-cell epitope;	
KW	Class I major histocompatibility complex allele; MHC; prostate cancer;	
KW	tumour; antigen presenting cell.	
OS		
XX	Homo sapiens.	
XX		
PN	US2003185830-A1.	
XX		
PD	02-OCT-2003.	

XX	12-NOV-2002; 2002US-00294025.	
PF		
XX	25-FEB-1997; 97US-00806099.	
PR	01-AUG-1997; 97US-00904804.	
PR	09-FEB-1998; 98US-00020956.	
PR	25-FEB-1998; 98US-00030607.	
PR	14-JUL-1998; 98US-00115453.	
PR	23-SEP-1998; 98US-00159812.	
PR	15-JAN-1999; 99US-00232149.	
PR	09-APR-1999; 99US-00288946.	
PR	13-JUL-1999; 99US-00352616.	
PR	12-NOV-1999; 99US-00439313.	
PR	18-NOV-1999; 99US-00443686.	
PR	14-JAN-2000; 2000US-00483672.	
PR	27-MAR-2000; 2000US-00536857.	
PR	09-MAY-2000; 2000US-00568100.	
PR	12-MAY-2000; 2000US-00570737.	
PR	13-JUN-2000; 2000US-00593793.	
PR	27-JUN-2000; 2000US-00605783.	
PR	09-AUG-2000; 2000US-00636215.	
PR	29-AUG-2000; 2000US-00651236.	
PR	06-SEP-2000; 2000US-00657279.	
PR	02-OCT-2000; 2000US-00679426.	
PR	10-OCT-2000; 2000US-00685166.	
PR	09-NOV-2000; 2000US-00709729.	
PR	12-JAN-2001; 2001US-00759143.	
PR	09-FEB-2001; 2001US-00780669.	
PR	09-MAY-2001; 2001US-00852911.	
PR	29-JUN-2001; 2001US-00895814.	
PR	10-DEC-2001; 2001US-00012896.	
PR	09-MAY-2002; 2002US-00144678.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolck JA, Kalos MD;	
XX	WPI; 2003-756193/71.	
DR		
XX		
PT	New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.	
PT		
XX		
PS	Example 3; Page; 101pp; English.	
XX		
CC	The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The	
CC	peptides comprise a fragment ADBI3563 of that contain naturally processed	
CC	T-cell epitopes for 3 class I major histocompatibility complex (MHC)	
CC	alleles. ADBI3563 is a polypeptide encoded by a human prostate specific	
CC	cDNA, one of 648 disclosed as new. Also included are nucleic acids	
CC	encoding the proteins and peptides, expression vectors, a host cell	
CC	transformed with the vector, an isolated antibody (or antigen binding	
CC	fragment) that specifically binds to the protein or peptide, detecting	
CC	the presence of a cancer in a patient (comprising contacting a patient	
CC	sample with a binding agent that binds to the peptides or a polypeptide	
CC	appearing as ADBI3558, detecting the amount of polypeptide that binds to	
CC	the agent and comparing the presence of cancer), a fusion protein	
CC	off value to determine the presence of cancer), a fusion protein	
CC	comprising the peptides or proteins, stimulating or expanding T cells	
CC	specific for a tumour protein comprising contacting T cells with the	
CC	peptides or the isolated T cell population, treating prostate cancer in a	
CC	patient comprising administering a composition comprising the peptides,	
CC	nucleic acids, antibodies or compounds, determining the presence of a	
CC	cancer in a patient and treating prostate cancer in a patient comprising	
CC	incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated	
CC	from a patient with the peptides or antigen presenting cells that express	
CC	(the peptides so that the T cells proliferate, and administering the	
CC	proliferated T cells to the patient. The peptides (or an oligonucleotide	
CC	that hybridises to nucleic acid encoding them), is used to detect the	
CC	presence of cancer in a patient. The peptides, nucleic acids encoding, or	
CC	antigen-presenting cells expressing the nucleic acid, are used to	
CC	stimulate or expand T cells specific for a tumour protein. The peptides,	

CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is one of the
CC disclosed human prostate specific cDNAs. Note: Except where otherwise
CC indicated, the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 10; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAATCGGTCACTCAAGGGCCCAACACAGCTGGAGCCAC 60
DB 1 ACGATTTCATTATCATGTAATCGGTCACTCAAGGGCCCAACACAGCTGGAGCCAC 60
QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GGGCCCTCAGATAGATCTGTAGCAAGAGAGAGAAACAACACTGATCTCTTCTG 180
DB 121 GGGCCCTCAGATAGATCTGTAGCAAGAGAGAGAAACAACACTGATCTCTTCTG 180
QY 181 CCACCCCTCGACCTTTGGAATCTCTCTGACCCCTTTAGAACAGGCTACTTAATATCTG 240
DB 181 CCACCCCTCGACCTTTGGAATCTCTCTGACCCCTTTAGAACAGGCTACTTAATATCTG 240
QY 241 CTAGAGAAAAGACCAACACGGGCTCTTACCATGAAGGCTCTCAGCTAAAT 300
DB 241 CTAGAGAAAAGACCAACACGGGCTCTTACCATGAAGGCTCTCAGCTAAAT 300
QY 301 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATATGGGGGAAGGCTCAATTTGCT 360
DB 301 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATATGGGGGAAGGCTCAATTTGCT 360
QY 361 CATTTCGTGTGTAAGTCAAGTCCAGGATGCCAGGGCCAGAGCGGGGCTGCTTCTTT 420
DB 361 CATTTCGTGTGTAAGTCAAGTCCAGGATGCCAGGGCCAGAGCGGGGCTGCTTCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACAACATCAAGTCA 480
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACAACATCAAGTCA 480
QY 481 TGTATCAATTCGATGAAGCTTGAAGGACCTGAACTTACCGATTCTCTTAAGGCAGCA 540
DB 481 TGTATCAATTCGATGAAGCTTGAAGGACCTGAACTTACCGATTCTCTTAAGGCAGCA 540
QY 541 GGCACGTTTGAAGTGGCAACATGCAGCAGCAAGATCAATGGAAACAACAGATGTTGC 600
DB 541 GGCACGTTTGAAGTGGCAACATGCAGCAGCAAGATCAATGGAAACAACAGATGTTGC 600
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
DB 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647

RESULT 11

ADG26174

ID ADG26174 standard; cDNA; 647 BP.

XX AC ADG26174;

XX AC ADG26174;

DT 26-FEB-2004 (first entry)

XX Human prostate-specific cDNA #300.

XX Human; prostate-specific polypeptide; gene; ss; prostate cancer;

XX cytostatic.

XX Homo sapiens.

OS

XX US2003157089-A1.
XX 21-AUG-2003.
XX 09-MAY-2002; 2002US-00144678.
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 18-NOV-1999; 99US-00439313.
XX 12-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00855814.
XX 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MB, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX WPI; 2003-777973/73.

XX New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.

XX Example 3; SEQ ID NO 308; 99pp; English.

XX The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 646; DB 10; Length 647;

XX Best Local Similarity 100.0%; Pred. No. 6.6e-200;

XX Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAATCGGTCACTCAAGGGCCCAACACAGCTGGAGCCAC 60

Db 1 ACGATTTTCATTTATCATGTAAATCGGTCACCTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAGAAACAAACACATGATCTCTTTCTG 180
Db 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAGAAACAAACACATGATCTCTTTCTG 180
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
Qy 241 CTAGAGAAAAGACCAACACGGCCCTCAAGAGATCTCTTACCATGAAGTCTCAGCTAATT 300
Db 241 CTAGAGAAAAGACCAACACGGCCCTCAAGAGATCTCTTACCATGAAGTCTCAGCTAATT 300
Qy 301 CTTGGCTAAGATGTGGGTTTCCATAGTTCCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTTCCATAGTTCCTGAATATGGGGGAAGGGTCAATTGCT 360
Qy 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCTAC 480
Db 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGGAACAAACAAACATCAAGTCTAC 480
Qy 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTTACCGATTCTTAAAGCAGCA 540
Db 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTTACCGATTCTTAAAGCAGCA 540
Qy 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600
Db 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600

RESULT 12
AEF66455

ID AEF66455 standard; cdna; 647 BP.

XX AEF66455;

XX 06-APR-2006 (first entry)

XX Human prostate tumor cdna clone P712P, SEQ ID 308.

XX Cytostatic; Gene Therapy; prostate tumor; ss.

XX Homo sapiens.

XX US2006024301-A1.

XX 02-FEB-2006.

XX 23-SEP-2005; 2005US-00234786.

XX 25-FEB-1997; 97US-00806099.

XX 01-AUG-1997; 97US-00904804.

XX 09-FEB-1996; 98US-00020956.

XX 25-FEB-1998; 98US-00030607.

XX 14-JUL-1998; 98US-00115453.

XX 23-SEP-1998; 98US-00159812.

XX 15-JAN-1999; 99US-00232149.

XX 09-APR-1999; 99US-00288946.

XX 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PA (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick IS;
PI Carter D, Li SX, Wang A, Skeiky YAW;
XX WPI; 2006-117603/12.
XX New fusion protein comprising a p50S polypeptide and an unrelated fusion
PT partner, useful for diagnosing, preventing, or treating cancer, such as
PT prostate cancer.
XX Example 3; SEQ ID NO 308; 78pp; English.
XX The present invention relates to prostate-specific fusion proteins and
CC DNA encoding sequences. The fusion proteins can be used for diagnosing,
CC preventing, or treating cancer, such as prostate cancer. The prostate-
CC specific proteins were isolated from a human prostate tumor cDNA library.
CC The present sequence is one such cDNA clone which was isolated in the
CC prostate-specific cDNA library. Note: The sequence data for this patent
CC did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 15; Length 647;

Best Local Similarity 100.0%; Pred. No. 6.6e-200; Indels 0; Gaps 0;

Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTTATCATGTAAATCGGTCACCTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60

Db 1 ACGATTTTCATTTATCATGTAAATCGGTCACCTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Db 61 TGCTCAGGGGAAGGTTTCATATAGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAGAAACAAACACATGATCTCTTTCTG 180

Db 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAGAAACAAACACATGATCTCTTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240

Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAAGACCAACCAACGGCCCTCAAGAGATCTCTTACCATGAAGTCTCAGCTAATT 300

Db 241 CTAGAGAAAAGACCAACCAACGGCCCTCAAGAGATCTCTTACCATGAAGTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420

Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420

Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACAAACATCAAGTCTAC 480

Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACAAACATCAAGTCTAC 480

Qy 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTTACCGATTCTTAAAGCAGCA 540

Db 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTTACCGATTCTTAAAGCAGCA 540

Qy 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600

Db 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600

Db 541 GGACCACTTTGAGTGGCAACAATGACAGCAGCAATCAATGGAACACACAGAAATGATTC 600
QY 601 AATGCTCTTTTCTCTGCTTCTGACTTGATATAAGGGACCGT 647
Db 601 AATGCTCTTTTCTCTGCTTCTGACTTGATATAAGGGACCGT 647

RESULT 13
ID ADB14484
XX ADB14484 standard; cDNA; 2577 BP.
AC ADB14484;
XX
DT 18-DEC-2003 (first entry)
XX Human prostate antigen P712P additional DNA sequence.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
PA (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Claim 6; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than

CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB13558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX

SQ Sequence 2577 BP; 826 A; 537 C; 506 G; 708 T; 0 U; 0 Other;

Query Match 93.0%; Score 600.8; DB 10; Length 2577;
Best Local Similarity 98.1%; Pred. No. 8e-185;
Matches 629; Conservative 0; Mismatches 8; Indels 4; Gaps 2;
QY 1 ACGATTTTCATTATCATGTAATCGGTGTCATCTCAAGGGGCCCAACACAGCTGGAGCCAC 60
Db 636 ACGATTTTCATTATCATGTAATCGGTGTCATCTCAAGGGGCCCAACACAGCTGGAGCCAC 695
QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTTACAGGATATAAA 120
Db 696 TGTCTAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTTACAGGATATAAA 755
QY 121 GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTCTG 180
Db 756 GGTGCTCCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTCTG 815
QY 181 CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 816 CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 875
QY 241 CTAGAGAAAAGACCAACCAACCGCTTCAAGAGGATCTTTTACCATGAAGGTTCTCAGCTAAT 300
Db 876 CTAGAGAAAAGACCAACCAACCGCTTCAAGAGGATCTTTTACCATGAAGGTTCTCAGCTAAT 935
QY 301 CTTGCTAAGATGTGGGTTTCCACATTAGTTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
Db 936 CTTGCTAAGATGTGGGTTTCCACATTAGTTTCTGAATATGGGGGAAGGTTCAATTTGCT 995
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTCTCTTGTCTT 420
Db 996 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTCTCTTGTCTT 1054
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGGAACAAAAACAACATCAAGTCTAC 480
Db 1055 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGGAACAAAAACAACATCAAGTCTAC 1111

QY 481 TGTATCAATTGCCATGAAGACTTGAGGACCTGAATCTACCGATTTCATCTTAAGCAGCA 540
 DB 1112 TGTATCAATTGCCATGAAGACTTGAGGACCTGAATCTACCGATTTCATCTTAAGCAGCA 1171
 QY 541 GGACCAAGTTTGAGTGGCAACAATGACAGCAGCAGCAATCAATGGAACAACACAGAAATGATTGC 600
 DB 1172 GGACCAAGTTTGAGTGGCAACAATGACAGCAGCAGCAATCAATGGAACAACACAGAAATGATTGC 1231
 QY 601 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTGATAAAAGGG 641
 DB 1232 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTGATAAAAGGG 1272

RESULT 14

ABV21571/c

ID ABV21571 standard; cDNA; 1481 BP.

AC ABV21571;

DT 13-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 21562.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW Pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

PN 23-AUG-2001.

PD 20-FEB-2001; 2001WO-US005171.

PR 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 3613; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 1481 BP; 364 A; 346 C; 314 G; 453 T; 0 U; 4 Other;

Query Match 92.8%; Score 599.2; DB 5; Length 1481;

Best Local Similarity 98.0%; Pred. No. 2e-184;

Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACAGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
 DB 1097 ACAGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 1038
 QY 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
 DB 1037 TGTCTCAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 978
 QY 121 GGNCCCTCACAGTATAGATCTGTAGCAAAAGAGAGAAAACAACATGATCTCTTTCTG 180
 DB 977 GGTGCTCTCACAGTATAGATCTGTAGCAAAAGAGAGAAAACAACATGATCTCTTTCTG 918
 QY 181 CCACCCCTCTGACCCCTTTTGGAACTCTCTGACCCCTTTAGAACAGCCTACTCTATATCTG 240
 DB 917 CCACCCCTCTGACCCCTTTTGGAACTCTCTGACCCCTTTAGAACAGCCTACTCTATATCTG 858
 QY 241 CTAGAGAAAAGACCAACACACGGGCTCAAAGGATCTTTTACCATGAAGGTTCTCAGCTAATT 300
 DB 857 CTAGAGAAAAGACCAACACACGGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAATT 798
 QY 301 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
 DB 797 CTTGGCTTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 738
 QY 361 CATTTTGTGTGATAAAGTTCAGGATGCCAGGGCCAGAGCAGGGGGCTGCTTGTCTTT 420
 DB 737 CATTTTGTGTGATAAAGTTCAGGATGCCAGGGCCAGAGCAGGGGGCTGCTGCTTT 679
 QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGGAACAAAACAACATCAAGTCAAC 480
 DB 678 GGGAAACAATGGCTGAGCATATAACCATAGG--TATGGGAACAAAACAACATCAAGTCAAC 622
 QY 481 TGTATCAATTTGCCATGAAGACTTTGAGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540
 DB 621 TGTATCAATTTGCCATGAAGACTTTGAGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 562
 QY 541 GGACCAAGTTTGAGTGGCAACAATGCACGACAGCAATCAATGGGAACAACAGAAATGATTGC 600
 DB 561 GGACCAAGTTTGAGTGGCAACAATGCACGACAGCAATCAATGGGAACAACAGAAATGATTGC 502
 QY 601 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTGATAAAAGGG 641
 DB 501 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTGATAAAAGGG 461

RESULT 15

ABV21485/c

ID ABV21485 standard; cDNA; 1481 BP.

XX AC ABV21485;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 21476.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW Pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

A (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 3587; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker; (j) (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1481 BP; 364 A; 346 C; 314 G; 453 T; 0 U; 4 Other;

Query Match 92.8%; Score 599.2; DB 5; Length 1481;

Query Match	Score	DB 3	Length
Best Local Similarity	92.8%	339.2	1481
Best Local Similarity	98.0%	Pred. No. 2e-184	

Best Local Similarity 98.0%; Rec. NO. 28-184,
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCAAGCTGGGAGCCAC 60

1097 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACCCACAGCTGGGAGCCAC 1038

61 TGCTCAGGGGAAGGTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

1037 TGGTCAGGGGAAGGTTTCATATGGGACCTTCTATACAGGATATAAA 978

121 G G G C C T C A C A G T A T A G A T C T G G T A G C A A G A A G A A C A A C A C T G A T C T C T T T C T G 180

977 CCTCCCTCAGCTATACATTCCTAGCACACGACACACACATCATTTCTTCTTG 918

[illegible]

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797 CTGGCTAAGATGTGGGTTCCACATTAGGTTCTGGATAATGGGGGAAGGGTCATTTTCCT 738

361 C A I I T T G T G T G G A T A T A G I C A G G A T G C C A G G G G C C A G A G C A G G G G C T G C T T G C T T T 420

37 CATTTGIGTGGATAAAGTCAGGATGCCCCAGGGGCGAGAGCAGGGGCGC-TCCTTT 679

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678 GGGAACAATGGCTGAGCATATAACCATAGG--TATGGGAACAAAAACATCAAAGTCAC 622

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621 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 562

541 GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAAACAGAAATGATTGC 600

561 GGACCACTTTGAGTGGCAACAATGCAGCAGCAGAAATCAATCGAAA

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501 AATGTCCTTTTCTCCTCCTCTCTGACTTGATAAAAGGG 461

Search completed: December 31, 2006, 12:54:16
Job time : 504.906 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:13:09 ; Search time 4165.51 Seconds
(without alignments)
9932.518 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattcatcatgta.....acttgataaaaggagccgt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_env.*
- 2: gb_pat.*
- 3: gb_ph.*
- 4: gb_pl.*
- 5: gb_pr.*
- 6: gb_ro.*
- 7: gb_sts.*
- 8: gb_sy.*
- 9: gb_un.*
- 10: gb_vi.*
- 11: gb_ov.*
- 12: gb_htg.*
- 13: gb_in.*
- 14: gb_om.*
- 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	2	BD242213 Compounds
2	646	100.0	647	2	AR237396 Sequence
3	646	100.0	647	2	AR278420 Sequence
4	646	100.0	647	2	AR367116 Sequence
5	646	100.0	647	2	AR371012 Sequence
6	646	100.0	647	2	AR400152 Sequence
7	646	100.0	647	2	AR405419 Sequence
8	646	100.0	647	2	AR439623 Sequence
9	646	100.0	647	2	AR563799 Sequence
10	646	100.0	647	2	AR598785 Sequence
11	646	100.0	647	2	AR605605 Sequence
12	646	100.0	647	2	AR656944 Sequence
13	646	100.0	647	2	AR716851 Sequence
14	646	100.0	647	2	AX106197 Sequence
15	646	100.0	647	2	AX106527 Sequence
16	646	100.0	647	2	AX140818 Sequence
17	646	100.0	647	2	AX200678 Sequence
18	646	100.0	647	2	AX267334 Sequence

19	602.4	93.3	1270	5	AY458019	Homo sapi
20	600.8	93.0	2084	5	AK056884	Homo sapi
21	600.8	93.0	2577	5	AY338953	Homo sapi
22	600.8	93.0	154078	5	CN5078FD	Human chr
23	599.2	92.8	1481	2	CQ489609	Sequence
24	599.2	92.8	1481	2	CQ489669	Sequence
25	599.2	92.8	1481	2	CQ489695	Sequence
26	599.2	92.8	1481	2	CQ489711	Sequence
27	599.2	92.8	1481	2	CQ490222	Sequence
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32	599.2	92.8	2577	2	AR278594	Sequence
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34	599.2	92.8	2577	2	AR405593	Sequence
35	599.2	92.8	2577	2	AR563973	Sequence
36	599.2	92.8	2577	2	AR588959	Sequence
37	599.2	92.8	2577	2	AR605779	Sequence
38	599.2	92.8	2577	2	AR657118	Sequence
39	599.2	92.8	2577	2	AR717025	Sequence
40	599.2	92.8	2577	2	AX200922	Sequence
41	599.2	92.8	2577	2	AX267578	Sequence
42	599.2	92.8	37981	5	AP000529	Homo sapi
43	599.2	92.8	42225	5	CR545463	Human DNA
44	599.2	92.8	176156	5	CNS08CCG	Human chr
45	583.4	90.3	813	7	BV557845	pr63f03.

ALIGNMENTS

BD242213 647 bp DNA linear PAT 17-JUL-2003
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.

BD242213
BD242213.1 GI:33051983

JP 2002520054-A/300.

Homo sapiens (human)

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 647)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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23-SEP-1998

15-JAN-1999

09-APR-1999

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FEATURES

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1..647

/organism="Homo sapiens"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAATAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 GNGCCTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
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Db 241 CTAGAGAAAAGAGACCAACACCGGCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
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Qy 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGGCTTT 420
Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC 480
Qy 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540
Db 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540
Qy 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTC 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTC 600
Qy 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAAGGGGACCGT 647

RESULT 3
AR278420
LOCUS
DEFINITION
Sequence 308 from patent US 6512094.
ACCESSION
AR278420.1 GI:29712666
VERSION
AR278420.1
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 647)
AUTHORS
Xiao, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL
Patent: US 6512094-A 308 28-JAN-2003;
Corixa Corporation; Seattle, WA
FEATURES
Location/Qualifiers
1..647
source
/organism="unknown"

/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAATAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 GNGCCTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATATCTG 240
Qy 241 CTAGAGAAAAGAGACCAACACCGGCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
Db 241 CTAGAGAAAAGAGACCAACACCGGCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
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Db 301 CTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGGCT 360
Qy 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGGCTTT 420
Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC 480
Qy 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540
Db 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540
Qy 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTC 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTC 600
Qy 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAAGGGGACCGT 647

RESULT 2
AR237396
LOCUS
DEFINITION
Sequence 308 from patent US 6465611.
ACCESSION
AR237396
VERSION
AR237396.1 GI:27282054
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 647)
AUTHORS
Xiao, J., Dillon, D.C. and Mitcham, J.L.
TITLE
Compounds for immunotherapy of prostate cancer and methods for
their use
JOURNAL
Patent: US 6465611-A 308 15-OCT-2002;
Corixa Corporation; Seattle, WA
FEATURES
Location/Qualifiers
1..647
source
/organism="unknown"
/mol_type="genomic DNA"
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ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%;	Score 646; DB 2; Length 647;
Best Local Similarity		100.0%;	Pred. No. 7.6e-202;
Matches 647; Conservative		0; Mismatches	0; Indels 0; Gaps 0;
QY	1	ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC	60
DB	1	ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC	60
QY	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAA	120
DB	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAA	120
QY	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAACACTGATCTCTTCTG	180
DB	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAACACTGATCTCTTCTG	180
QY	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
DB	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
QY	241	CTAGAGAAAGAACCAACACGGCCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
DB	241	CTAGAGAAAGAACCAACACGGCCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
QY	301	CTTGGCTAAGATGTGGTTTCCACATAGGTCTCTGATATATGGGGGAAGGTCATTTGCT	360
DB	301	CTTGGCTAAGATGTGGTTTCCACATAGGTCTCTGATATATGGGGGAAGGTCATTTGCT	360
QY	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
DB	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
QY	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAACAAAAACAACATCAAGTCTAC	480
DB	421	GGGAACAATGGCTGAGCATATAAACCATAGGTTATGGGAACAAAAACAACATCAAGTCTAC	480
QY	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
DB	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
QY	541	GGACCAAGTTTGTAGTGGCAACAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC	600
DB	541	GGACCAAGTTTGTAGTGGCAACAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC	600
QY	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
DB	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647

RESULT 5		AR371012		647 bp		DNA		linear		PAT 12-SEP-2003	
LOCUS		AR371012		Sequence 308 from patent US 6395278.		DEFINITION		AR371012		ACCESSION	
VERSION		AR371012.1		GI:34607905		KEYWORDS		Unknown.		SOURCE	
ORGANISM		Unknown.		Unclassified.		REFERENCE		1 (bases 1 to 647)		AUTHORS	
TITLE		Prostate specific fusion protein compositions		Patent: US 6395278-A 308 28-MAY-2002;		JOURNAL		Corixa Corporation; Seattle, WA		FEATURES	
source		1. .647		/organism="unknown"		/mol_type="genomic DNA"		ORIGIN			

Query Match		100.0%;	Score 646; DB 2; Length 647;
Best Local Similarity		100.0%;	Pred. No. 7.6e-202;
Matches 647; Conservative		0; Mismatches	0; Indels 0; Gaps 0;
QY	1	ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC	60
DB	1	ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGAGCCAC	60
QY	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAA	120
DB	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAA	120
QY	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAACACTGATCTCTTCTG	180
DB	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAACACTGATCTCTTCTG	180
QY	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
DB	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
QY	241	CTAGAGAAAGAACCAACACGGCCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
DB	241	CTAGAGAAAGAACCAACACGGCCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
QY	301	CTTGGCTAAGATGTGGTTTCCACATAGGTCTCTGATATATGGGGGAAGGTCATTTGCT	360
DB	301	CTTGGCTAAGATGTGGTTTCCACATAGGTCTCTGATATATGGGGGAAGGTCATTTGCT	360
QY	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
DB	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
QY	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAACAAAAACAACATCAAGTCTAC	480
DB	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAACAAAAACAACATCAAGTCTAC	480
QY	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
DB	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
QY	541	GGACCAAGTTTGTAGTGGCAACAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC	600
DB	541	GGACCAAGTTTGTAGTGGCAACAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC	600
QY	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
DB	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647

RESULT 4		AR367116		647 bp		DNA		linear		PAT 12-SEP-2003	
LOCUS		AR367116		Sequence 308 from patent US 6329505.		DEFINITION		AR367116		ACCESSION	
VERSION		AR367116.1		GI:34600091		KEYWORDS		Unknown.		SOURCE	
ORGANISM		Unknown.		Unclassified.		REFERENCE		1 (bases 1 to 647)		AUTHORS	
TITLE		Compositions and methods for therapy and diagnosis of prostate cancer		Patent: US 6329505-A 308 11-DEC-2001;		JOURNAL		Corixa Corporation; Seattle, WA		FEATURES	
source		1. .647		/organism="unknown"		/mol_type="genomic DNA"		ORIGIN			

Query Match 100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.6e-202; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0;

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Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120
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Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAACACTGATCTCTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAACACTGATCTCTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAAGACCAACACCGGCTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATT 300
Db 241 CTAGAGAAAAGACCAACACCGGCTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGCGGTTCCACATTAGGTTCTGNAATATGGGGGAAGGTTCAATTGCT 360
Db 301 CTTGGCTAAGATGCGGTTCCACATTAGGTTCTGNAATATGGGGGAAGGTTCAATTGCT 360

Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420

Qy 421 GGGAAACAATGCTGAGCATATAACCATAGGTTATGGGAAACAAAACAACATCAAGTCAC 480
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Qy 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAACTACCGATTTCATCTTAAAGCAGCA 540
Db 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAACTACCGATTTCATCTTAAAGCAGCA 540

Qy 541 GGACCAAGTTGAGTGGCAACATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600
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Qy 601 AATGTCCTTTTTTCTCCTGCTCTGACTTGATATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTCTCCTGCTCTGACTTGATATAAAAGGGGACCGT 647

RESULT 6
LOCUS AR400152 647 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 308 from patent US 6620922.
ACCESSION AR400152
VERSION AR400152.1 GI:40143258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 647)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6620922-A 308 16-SEP-2003;
Corixa Corporation; Seattle, WA
FEATURES
source 1. .647
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7.6e-202; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0;

Qy 1 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCCAACACACAGCTGGGAGCCAC 60

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Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAACACTGATCTCTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAACACTGATCTCTTCTG 180

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Qy 301 CTTGGCTAAGATGCGGTTCCACATTAGGTTCTGNAATATGGGGGAAGGTTCAATTGCT 360
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Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420

Qy 421 GGGAAACAATGCTGAGCATATAACCATAGGTTATGGGAAACAAAACAACATCAAGTCAC 480
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Qy 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAACTACCGATTTCATCTTAAAGCAGCA 540
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Qy 541 GGACCAAGTTGAGTGGCAACATGAGCAGCAGAGATCAATGGAAACAACAGATGATTGC 600
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Qy 601 AATGTCCTTTTTTCTCCTGCTCTGACTTGATATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTCTCCTGCTCTGACTTGATATAAAAGGGGACCGT 647

RESULT 7
LOCUS AR405419 647 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 308 from patent US 6630305.
ACCESSION AR405419
VERSION AR405419.1 GI:40154256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 647)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 308 07-OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;
FEATURES
source 1. .647
/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7,6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY 61 TGCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTTATACAGATATAA 120
DB 61 TGCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTTATACAGATATAA 120

QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240

QY 241 CTAGAGAAAGAACCAACACGGCTCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300
DB 241 CTAGAGAAAGAACCAACACGGCTCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300

QY 301 CTTGGCTAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420

QY 421 GGAACAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACATCAAGTCTAC 480
DB 421 GGAACAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACATCAAGTCTAC 480

QY 481 TGTATCAATTTGCTGAGTGGGACCTGAACTCTACCGATTCTCTTAAAGGAGCA 540
DB 481 TGTATCAATTTGCTGAGTGGGACCTGAACTCTACCGATTCTCTTAAAGGAGCA 540

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DB 541 GGACCAAGTTTGAAGTGGCAACCAATGACGACGAGATCAATGGAACCAACAGATGATTC 600

QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATATAAAGGGACCGT 647
DB 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATATAAAGGGACCGT 647

RESULT 8

AR439623
LOCUS 647 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 308 from patent US 6664377.
ACCESSION AR439623
VERSION AR439623.1 GI:42665532
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Xu, J.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6664377-A 308 16-DEC-2003;
Corixa Corporation; Seattle, WA;
WOX;
FEATURES
source Location/Qualifiers
1. .647
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 7,6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY 61 TGCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTTATACAGATATAA 120
DB 61 TGCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTTATACAGATATAA 120

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DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180

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DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240

QY 241 CTAGAGAAAGAACCAACACGGCTCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300
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QY 301 CTTGGCTAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420

QY 421 GGAACAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACATCAAGTCTAC 480
DB 421 GGAACAATGGCTGAGCATATAACCATAGTTTATGGGAAACAAACATCAAGTCTAC 480

QY 481 TGTATCAATTTGCTGAGTGGGACCTGAACTCTACCGATTCTCTTAAAGGAGCA 540
DB 481 TGTATCAATTTGCTGAGTGGGACCTGAACTCTACCGATTCTCTTAAAGGAGCA 540

QY 541 GGACCAAGTTTGAAGTGGCAACCAATGACGACGAGATCAATGGAACCAACAGATGATTC 600
DB 541 GGACCAAGTTTGAAGTGGCAACCAATGACGACGAGATCAATGGAACCAACAGATGATTC 600

QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATATAAAGGGACCGT 647
DB 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATATAAAGGGACCGT 647

RESULT 9

AR563799
LOCUS 647 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 308 from patent US 6759515.
ACCESSION AR563799
VERSION AR563799.1 GI:53978850
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6759515-A 308 06-JUL-2004;
Corixa Corporation; Seattle, WA
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AUTHORS		Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.		AUTHORS		Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.		AUTHORS	
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JOURNAL Patent: US 6943236-A 308 13-SEP-2005;

Corixa Corporation; Seattle, WA

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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Hominidae; Homo.

REFERENCE
1
AUTHORS Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLE Compositions and methods for wt1 specific immunotherapy
JOURNAL Patent: WO 0125273-A 335 12-APR-2001;

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Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION AX106527.1 GI:13922205
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Hominidae; Homo.

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AUTHORS Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.

TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 308 12-APR-2001;
CORIXA CORPORATION (US)
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SUMMARIES

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ALIGNMENTS

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; Sequence 308, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

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; OTHER INFORMATION: n = A,T,C or G

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; Patent No. 6395278

GENERAL INFORMATION:

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0

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; NAME/KEY: misc feature

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; OTHER INFORMATION: n = A,T,C or G

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Db 481 TGTATCAATGCCATGAAGCTTGAGGACCTGAATCTACCGATTTCATCTTTAAGGCAGCA 540
Qy 541 GGACAGCTTTGAGTGGCAACAATGAGCAGCAGCAATCAATGGAACACAGATGATTGC 600
Db 541 GGACAGCTTTGAGTGGCAACAATGAGCAGCAGCAATCAATGGAACACAGATGATTGC 600
Qy 601 AATGTCCTTTTTTTCTCTGCTTCTGATGATGATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTGCTTCTGATGATGATAAAAGGGGACCGT 647
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RESULT 3

US-09-232-149A-308
; Sequence 308, Application US/09232149A
; Patent No. 6465611

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 308

; LENGTH: 647

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(647)

; OTHER INFORMATION: n = A,T,C or G

US-09-232-149A-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGGGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGGGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATCGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GGGGCTTCACAGTATAGATCTGGTACAAAGAGAGAAACAACAACATGATCTCTTTCTG 180
Db 121 GGGGCTTCACAGTATAGATCTGGTACAAAGAGAGAAACAACAACATGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACAAGGCTCAAGGATCTCTTACCATGAAGGCTCTAGCTAATTT 300
Db 241 CTAGAGAAAGACCAACAAGGCTCAAGGATCTCTTACCATGAAGGCTCTAGCTAATTT 300
QY 301 CTGGGCTTAAGATCTGGGTTCCACATTAAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTGGGCTTAAGATCTGGGTTCCACATTAAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGAACAATGGCTTGAGATATAACCATAGGTTATGGGGAACAAACAACATCAAGTCTAC 480
Db 421 GGAACAATGGCTTGAGATATAACCATAGGTTATGGGGAACAAACAACATCAAGTCTAC 480
QY 481 TGATCAATTTGCTGATGAAGCTTGGGACCTCAATCTACCGATTCTTAAAGGACGCA 540
Db 481 TGATCAATTTGCTGATGAAGCTTGGGACCTCAATCTACCGATTCTTAAAGGACGCA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 600
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGACCGT 647
Db 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGACCGT 647
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RESULT 4

US-09-636-215-308
; Sequence 308, Application US/09636215
; Patent No. 6620922

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 308

LENGTH: 647

TYPE: DNA

ORGANISM: Homo sapien

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-308

Query Match 100.0%; Score 646; DB 3; Length 647;

Best Local Similarity 100.0%; Pred. No. 2.1e-206;

Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACGATTTTCATTATCATGTAAATCGGTGCTCAAGGGGCCCAACACACAGCTGGGACCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGTGCTCAAGGGGCCCAACACACAGCTGGGACCCAC 60
QY 61 TCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
Db 61 TCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GGGGCTTCACAGTATAGATCTGGTACAAAGAGAGAAACAACAACATGATCTCTTTCTG 180
Db 121 GGGGCTTCACAGTATAGATCTGGTACAAAGAGAGAAACAACAACATGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACAAGGCTCAAGGCTCAAGGATCTCTTACCATGAAGGCTCTAGCTAATTT 300
Db 241 CTAGAGAAAGACCAACAAGGCTCAAGGCTCAAGGATCTCTTACCATGAAGGCTCTAGCTAATTT 300
QY 301 CTGGGCTTAAGATCTGGGTTCCACATTAAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTGGGCTTAAGATCTGGGTTCCACATTAAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GGAACAATGGCTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 480
Db 421 GGAACAATGGCTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 480
QY 481 TGATCAATTTGCTGATGAAGCTTGGGACCTCAATCTACCGATTCTTAAAGGACGCA 540
Db 481 TGATCAATTTGCTGATGAAGCTTGGGACCTCAATCTACCGATTCTTAAAGGACGCA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGATCAATGGAACAAACAAGATGATTC 600
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGACCGT 647
Db 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATGATAAAGGGACCGT 647
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RESULT 5

US-09-685-166A-308

; Sequence 308, Application US/09685166A

; Patent No. 6630305

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACGATTTTCATATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTTCTG 180
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 240
Qy 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Qy 361 CATTTTGTGTGGATTAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATTAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTGCTTT 420
Qy 421 GGGAAACAATGGCTGAGCATATAACATAGGTTATGGGGAACAAACACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACATAGGTTATGGGGAACAAACACATCAAAAGTCAC 480
Qy 481 TGTATCAATTGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540
Db 481 TGTATCAATTGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540
Qy 541 GGACACAGTTTGAGTGGCAACAATGCAGCAGAGATCAATGGAACACACAGATGATTGC 600
Db 541 GGACACAGTTTGAGTGGCAACAATGCAGCAGAGATCAATGGAACACACAGATGATTGC 600
Qy 601 AATGTCCTTTTTTTCTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647

RESULT 6
US-09-688-489-308
; Sequence 308, Application US/09688489

; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-688-489-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACGATTTTCATATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACATGATCTCTTTCTG 180
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 240
Qy 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCCTCAGCTAATT 300
Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Qy 361 CATTTTGTGTGGATTAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATTAAGTCAGGATGCCAGGGGCCAGAGAGGGGGCTGCTTGCTTT 420
Qy 421 GGGAAACAATGGCTGAGCATATAACATAGGTTATGGGGAACAAACACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACATAGGTTATGGGGAACAAACACATCAAAAGTCAC 480
Qy 481 TGTATCAATTGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540
Db 481 TGTATCAATTGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540
Qy 541 GGACACAGTTTGAGTGGCAACAATGCAGCAGAGATCAATGGAACACACAGATGATTGC 600
Db 541 GGACACAGTTTGAGTGGCAACAATGCAGCAGAGATCAATGGAACACACAGATGATTGC 600
Qy 601 AATGTCCTTTTTTTCTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647

RESULT 7
US-09-679-426-308


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; Sequence 308, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: n = A,T,C or G
; US-09-679-426-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.le-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
QY 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
DB 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300
DB 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300
QY 301 CTTGGCTTAAGATGTGGTTCACATTAAGTTCTGAATATGGGGGAGAGGTCATTTGCT 360
DB 301 CTTGGCTTAAGATGTGGTTCACATTAAGTTCTGAATATGGGGGAGAGGTCATTTGCT 360
QY 361 CATTTTGTGTGTGATAAAGTCAAGATGCCAGGGGCCAGAGCAGAGGGGCTGCTCTCTTT 420
DB 361 CATTTTGTGTGTGATAAAGTCAAGATGCCAGGGGCCAGAGCAGAGGGGCTGCTCTCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCTAC 480
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCTAC 480

; Sequence 308, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: n = A,T,C or G
; US-09-759-143-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.le-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
QY 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
DB 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300
DB 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300

; Sequence 308, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: n = A,T,C or G
; US-09-759-143-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.le-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB 1 ACAGATTTTCATTATCATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 60
QY 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
DB 61 TGTCTAGGGAAGGTTCAATATGAGGACTTTCTACTGCGGTCACCTCAAGGGGCCAACACACAGCTGGAGCCAC 120
QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300
DB 241 CTAGAGAAAGAGCAACACAGGCTCTTACAGGATCTCTTACCATGAAAGGTTCTACGCTAAATTT 300
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; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-657-279-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACGATTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB      1  ACGATTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY      61  TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB      61  TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

QY      121  GNGGCCTCAGTATAGATCTGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
DB      121  GNGGCCTCAGTATAGATCTGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180

QY      181  CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
DB      181  CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240

QY      241  CTAGAGAAAGACCAACACGGGCTCAAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300
DB      241  CTAGAGAAAGACCAACACGGGCTCAAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300

QY      301  CTTGGCTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB      301  CTTGGCTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGTCATTTGCT 360

QY      361  CATTTTGTGTGGATAAGTCAAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420
DB      361  CATTTTGTGTGGATAAGTCAAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420

QY      421  GGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACCAACATCAAGTCTAC 480
DB      421  GGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACCAACATCAAGTCTAC 480

QY      481  TGTATCAATTGCCATGAAGCTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540
DB      481  TGTATCAATTGCCATGAAGCTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540

QY      541  GGACCAAGTTTGAGTGGCAACATGCAGCAGCAGATCAATGGAACCAACAGATGATTCG 600
DB      541  GGACCAAGTTTGAGTGGCAACATGCAGCAGCAGATCAATGGAACCAACAGATGATTCG 600

QY      601  AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
DB      601  AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
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RESULT 11

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US-10-012-896-308
; Sequence 308, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
```

```
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACGATTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
DB      1  ACGATTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY      61  TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB      61  TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

QY      121  GNGGCCTCAGTATAGATCTGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180
DB      121  GNGGCCTCAGTATAGATCTGTAGCAAGAGAGAAACAAACACTGATCTCTTTCTG 180

QY      181  CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
DB      181  CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240

QY      241  CTAGAGAAAGACCAACACGGGCTCAAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300
DB      241  CTAGAGAAAGACCAACACGGGCTCAAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT 300

QY      301  CTTGGCTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGTCATTTGCT 360
DB      301  CTTGGCTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGTCATTTGCT 360

QY      361  CATTTTGTGTGGATAAGTCAAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420
DB      361  CATTTTGTGTGGATAAGTCAAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420

QY      421  GGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACCAACATCAAGTCTAC 480
DB      421  GGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACCAACATCAAGTCTAC 480

QY      481  TGTATCAATTGCCATGAAGCTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540
DB      481  TGTATCAATTGCCATGAAGCTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540

QY      541  GGACCAAGTTTGAGTGGCAACATGCAGCAGCAGATCAATGGAACCAACAGATGATTCG 600
DB      541  GGACCAAGTTTGAGTGGCAACATGCAGCAGCAGATCAATGGAACCAACAGATGATTCG 600
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Qy 601 AATGTCCTTTTCTCTGCTTCTGACTTGAATAAAAGGGACCGT 647
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RESULT 12

US-10-144-678A-308
; Sequence 308, Application US/10144678A

; Patent No. 7033827

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Hepler, William T.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals y de Bassols, Carlota

; APPLICANT: Foy, Teresa M.

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Deng, Ta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C28

; CURRENT APPLICATION NUMBER: US/10/144,678A

; CURRENT FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 308

; LENGTH: 647

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 123

; OTHER INFORMATION: n = A,T,C or G

US-10-144-678A-308

Query Match 100.0%; Score 646; DB 5; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0

Qy 1 ACGATTTTCATTATCATGTAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GGGGCTCACAGTATAGTCTGTAGCAAGAAAGAAAGAAACAAACACATGATCTTTCTG 180
Db 121 GGGGCTCACAGTATAGTCTGTAGCAAGAAAGAAAGAAACAAACACATGATCTTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAAACAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAAGACCAACACAGCGCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
Db 241 CTAGAGAAAAGACCAACACAGCGCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATATGGGGGAAGGGTCAATTGGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATATGGGGGAAGGGTCAATTGGCT 360
Qy 361 CATTTTGTGTGATTAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTTT 420
Db 361 CATTTTGTGTGATTAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTTT 420
Qy 421 GGGAAACAATGCTGAGCATATAACCATAGGTTTATGGGGAAACAAACCAACATCAAGTCAC 480
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Qy 481 TGTATCAATTTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTCTTAAAGGCAGCA 540
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Qy 601 AATGTCCTTTTCTCTGCTTCTGACTTTGATAAAAGGGACCGT 647
Db 601 AATGTCCTTTTCTCTGCTTCTGACTTTGATAAAAGGGACCGT 647

RESULT 13

US-09-636-215-552

; Sequence 552, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 552

; LENGTH: 2577

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-552

Query Match 92.8%; Score 599.2; DB 3; Length 2577;
Best Local Similarity 98.0%; Pred. No. 2.6e-190;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 1 ACGATTTTCATTATCATGTAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 636 ACGATTTTCATTATCATGTAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 695
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C20

; CURRENT APPLICATION NUMBER: US/09/679,426

; CURRENT FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 895

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 552

; LENGTH: 2577

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-679-426-552

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Query Match      92.8%; Score 599.2; DB 3; Length 2577;
Best Local Similarity 98.0%; Pred. No. 2.6e-190;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY      1  ACGATTTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACCCACAGCTGGGAGCCAC 60
Db      |||
QY      61  TGCTCAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db      |||
QY      696  TGCTCAGGGGAAGGTTTCATATGGGACTTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 755
Db      |||
QY      121  GGNGCCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACTGATCTCTTCTG 180
Db      |||
QY      756  GGTGCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACTGATCTCTTCTG 815
Db      |||
QY      181  CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 240
Db      |||
QY      816  CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 875
Db      |||
QY      241  CTAGAGAAAGAACCAACACGGCCCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAATT 300
Db      |||
QY      876  CTAGAGAAAGAACCAACACGGCCCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAATT 935
Db      |||
QY      301  CTGGCTAAGATGTGGGTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360
Db      |||
QY      936  CTGGCTAAGATGTGGGTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 995
Db      |||
QY      361  CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420
Db      |||
QY      996  CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTGCTTT 1054
Db      |||
QY      421  GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAAGTCAC 480
Db      |||
QY      1055  GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAAGTCAC 1111
Db      |||
QY      481  TGTATCAATGGCATGAAGACTTTGAGGACCTGAATCTACCGATTCATCTTAAGGCAGCA 540
Db      |||
QY      1112  TGTATCAATGGCATGAAGACTTCGAGGACCTGAATCTACCGATTCATCTTAAGGCAGCA 1171
Db      |||
QY      541  GGACCAATTTGAGTGGCAACAAATGAGCAGCAGAGATCAATGGAACAAACAGAAATGATGC 600
Db      |||
QY      1172  GGACCAATTTGAGTGGCAACAAATGAGCAGCAGAGATCAATGGAACAAACAGAAATGATGC 1231
Db      |||
QY      601  AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 641
Db      |||
QY      1232  AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1272
Db      |||
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Search completed: December 31, 2006, 12:31:09

Job time : 153.014 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:18:37 ; Search time 122.772 Seconds
(without alignments)
8016.516 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	525	100.0	526	3	US-09-439-313-311 Sequence 311, App
2	525	100.0	526	3	US-09-352-616A-311 Sequence 311, App
3	525	100.0	526	3	US-09-232-149A-311 Sequence 311, App
4	525	100.0	526	3	US-09-636-215-311 Sequence 311, App
5	525	100.0	526	3	US-09-685-166A-311 Sequence 311, App
6	525	100.0	526	3	US-09-688-489-311 Sequence 311, App
7	525	100.0	526	3	US-09-679-426-311 Sequence 311, App
8	525	100.0	526	3	US-09-759-143-311 Sequence 311, App
9	525	100.0	526	3	US-09-651-236-311 Sequence 311, App
10	525	100.0	526	3	US-09-657-279-311 Sequence 311, App
11	525	100.0	526	3	US-10-012-896-311 Sequence 311, App
12	525	100.0	526	5	US-10-144-678A-311 Sequence 311, App
C 13	469.2	89.4	3434	3	US-09-439-313-476 Sequence 476, App
C 14	469.2	89.4	3434	3	US-09-636-215-476 Sequence 476, App
C 15	469.2	89.4	3434	3	US-09-685-166A-476 Sequence 476, App
C 16	469.2	89.4	3434	3	US-09-679-426-476 Sequence 476, App
C 17	469.2	89.4	3434	3	US-09-759-143-476 Sequence 476, App
C 18	469.2	89.4	3434	3	US-09-651-236-476 Sequence 476, App
C 19	469.2	89.4	3434	3	US-09-657-279-476 Sequence 476, App
C 20	469.2	89.4	3434	3	US-10-012-896-476 Sequence 476, App
C 21	469.2	89.4	3434	5	US-10-144-678A-476 Sequence 476, App
C 22	261.6	49.8	2414	3	US-09-439-313-475 Sequence 475, App
C 23	261.6	49.8	2414	3	US-09-636-215-475 Sequence 475, App

ALIGNMENTS

RESULT 1

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US-09-439-313-311
; Sequence 311, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-311

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Query Match 100.0%; Score 525; DB 3; Length 526;

Best Local Similarity 100.0%; Pred. No. 9.5e-125; Mismatches 0; Indels 0; Gaps 0;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60

Db 1 CAAATTTGAGCCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCAATTAATGATCCATAAATATATATCTA 120

Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCAATTAATGATCCATAAATATATATCTA 120

Qy 121 CATTTCACGATTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

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C 25 261.6 49.8 2414 3 US-09-679-426-475 Sequence 475, App
C 26 261.6 49.8 2414 3 US-09-759-143-475 Sequence 475, App
C 27 261.6 49.8 2414 3 US-09-651-236-475 Sequence 475, App
C 28 261.6 49.8 2414 3 US-09-657-279-475 Sequence 475, App
C 29 261.6 49.8 2414 3 US-10-012-896-475 Sequence 475, App
C 30 261.6 49.8 2414 5 US-10-144-678A-475 Sequence 475, App
C 31 109 20.8 1594 3 US-09-439-313-474 Sequence 474, App
C 32 109 20.8 1594 3 US-09-636-215-474 Sequence 474, App
C 33 109 20.8 1594 3 US-09-685-166A-474 Sequence 474, App
C 34 109 20.8 1594 3 US-09-679-426-474 Sequence 474, App
C 35 109 20.8 1594 3 US-09-759-143-474 Sequence 474, App
C 36 109 20.8 1594 3 US-09-651-236-474 Sequence 474, App
C 37 109 20.8 1594 3 US-09-657-279-474 Sequence 474, App
C 38 109 20.8 1594 3 US-10-012-896-474 Sequence 474, App
C 39 109 20.8 1594 5 US-10-144-678A-474 Sequence 474, App
C 40 43.2 8.2 317366 3 US-09-949-016-16001 Sequence 16001, A
C 41 42.2 8.1 101674 3 US-09-949-016-12033 Sequence 12033, A
C 42 42.2 8.0 50000 3 US-09-662-254B-26 Sequence 26, Appli
C 43 42 8.0 1664976 3 US-08-916-421B-1 Sequence 1, Appli
C 44 42 8.0 1664976 3 US-09-692-570-1 Sequence 1, Appli
C 45 41.8 8.0 109925 3 US-09-949-016-13210 Sequence 13210, A

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Db 121 CATTTACAGCAATTTAAATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTTAATAA 180
Qy 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240
Db 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCTCTGAGGCTTCTGAGGCTTCTGAGGCTGAGATCTTGAATTGC 420
Db 361 TCTCTTTACAGGAGCTCTCTGAGGCTTCTGAGGCTTCTGAGGCTGAGATCTTGAATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Qy 481 AGTTCTATAAACTGTAGTACTTATTTAAATCCCAAGCAGCT 526
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RESULT 2

US-09-352-616A-311
; Sequence 311, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yucui
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Db 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Qy 121 CATTTACAGCAATTTAAATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTTAATAA 180
Db 121 CATTTACAGCAATTTAAATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTTAATAA 180
Qy 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240

Db 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCTCTGAGGCTTCTGAGGCTTCTGAGGCTGAGATCTTGAATTGC 420
Db 361 TCTCTTTACAGGAGCTCTCTGAGGCTTCTGAGGCTTCTGAGGCTGAGATCTTGAATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Qy 481 AGTTCTATAAACTGTAGTACTTATTTAAATCCCAAGCAGCT 526
Db 481 AGTTCTATAAACTGTAGTACTTATTTAAATCCCAAGCAGCT 526

RESULT 3

US-09-232-149A-311
; Sequence 311, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Qy 61 TTTTGAGCTTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Db 61 TTTTGAGCTTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Qy 121 CATTTACAGCAATTTAAATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTTAATAA 180
Db 121 CATTTACAGCAATTTAAATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTTAATAA 180
Qy 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240
Db 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Db 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526

RESULT 4

US-09-636-215-311
; Sequence 311, Application US/09636215
; Patent No. 6620922

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G

US-09-636-215-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATCTA 120
QY 121 CATTTACAGATTAAATGCTTTGAGCATGAATATAGCTACAGGGAGCTAAATAA 180
Db 121 CATTTACAGATTAAATGCTTTGAGCATGAATATAGCTACAGGGAGCTAAATAA 180
QY 181 ATTAACATCGGAATAAGATTGTCTCTTAAATATAATCTACAAGAGACCTTTGATATTG 240

Db 181 ATTAACATCGGAATAAGATTGTCTCTTAAATATAATCTACAAGAGACCTTTGATATTG 240
QY 241 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATCGGAA 300
Db 241 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATCGGAA 300
QY 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526

RESULT 5

US-09-685-166A-311
; Sequence 311, Application US/09685166A
; Patent No. 6630305

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G

US-09-685-166A-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATCTA 120


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QY 121 CAATTTACAGCATTTAAATGTTTACGATGAATATTTAGCTACAGGGAGCTAAATAA 180
DB 121 CAATTTACAGCATTTAAATGTTTACGATGAATATTTAGCTACAGGGAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCCTTAAATAATAATCTACAAGAGACTTTTGATTTG 240
DB 181 ATTAACATGGAATAAAGATTGTCCTTAAATAATAATCTACAAGAGACTTTTGATTTG 240
QY 241 TTTTTCACAGCTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGAACTATGGGA 300
DB 241 TTTTTCACAGCTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGAACTATGGGA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGTGATCTGATCAAGTATAA 480
DB 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGTGATCTGATCAAGTATAA 480
QY 421 ACAGCAAGACTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
DB 421 ACAGCAAGACTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
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RESULT 8

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US-09-759-143-311
; Sequence 311, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
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US-09-759-143-311
Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGCCATTTC 60
DB 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGCCATTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTCTAAAGAGGCAATTAATGATCCATAAATATATATTATCTA 120
DB 61 TTTTGACGTTTTCTCTAAACTCTAAAGAGGCAATTAATGATCCATAAATATATATTATCTA 120
QY 121 CATTTACACATTTAAATGTTTCTAGCATGAAATATTAAGCTACAGGGAGCTAAATAA 180
DB 121 CATTTACACATTTAAATGTTTCTAGCATGAAATATTAAGCTACAGGGAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCCTTAAATAATAATCTACAAGAGACTTTTGATTTG 240
DB 181 ATTAACATGGAATAAAGATTGTCCTTAAATAATAATCTACAAGAGACTTTTGATTTG 240
QY 241 TTTTTCACAGCTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGAACTATGGGA 300
DB 241 TTTTTCACAGCTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGAACTATGGGA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGTGATCTGATCAAGTATAA 480
DB 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGTGATCTGATCAAGTATAA 480
QY 421 ACAGCAAGACTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
DB 421 ACAGCAAGACTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
QY 481 AGTTCTATAAATGTTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAATGTTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
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RESULT 9

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US-09-651-236-311
; Sequence 311, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
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; OTHER INFORMATION: n = A,T,C or G
US-09-651-236-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
Qy 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Qy 181 ATTAACATGGAATAAAGATTGCTTAAATATTAATCTACAAGAAGCTTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGCTTAAATATTAATCTACAAGAAGCTTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Qy 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCCAAAGCACAGT 526
Db 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCCAAAGCACAGT 526
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RESULT 10
US-09-657-279-311
; Sequence 311, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-657-279-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
Qy 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Qy 181 ATTAACATGGAATAAAGATTGCTTAAATATTAATCTACAAGAAGCTTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGCTTAAATATTAATCTACAAGAAGCTTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Qy 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCCAAAGCACAGT 526
Db 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCCAAAGCACAGT 526
```

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RESULT 11
US-10-012-896-311
; Sequence 311, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
```


Qy 481 AGTTCATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
|||||
Db 481 AGTTCATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 13

US-09-439-313-476/c
; Sequence 476, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-476

Query Match 89.4%; Score 469.2; DB 3; Length 3434;
Best Local Similarity 97.9%; Pred. No. 2.9e-110;
Matches 507; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
Qy 1 CAAATTTGAGCCAAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 3062 CAAATTTGAGCCAAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 3003
Qy 61 TTTTGACGTTTCTCTAACTACTAAAGGCAATTAATGATCCATAAATATATATCTA 120
Db 3002 TTTTGACGTTTCTCTAACTACTAAAGGCAATTAATGATCCATAAATATATATCTA 2943
Qy 121 CATTTACAGCATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180
Db 2942 CATTTACAGCATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 2883
Qy 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240
Db 2882 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 2823
Qy 241 TTTTTCACAAGTGAAGCATCTTATAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 300
Db 2822 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 2763
Qy 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 2762 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 2703
Qy 361 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATCTTGAATTCG 420
Db 2702 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATCTTGAATTCG 2643
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Db 2642 ATAGC-AGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATC-AGTATAA 2585
Qy 481 AGTTCATAAACTGTAGTNTACTTATTTTAAATCCCAAA 518
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Db 2584 AGTTCATAAACTGTAGT-TACTTATTTTAAATCCCAA 2548

RESULT 14

US-09-636-215-476/c
; Sequence 476, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-476

Query Match 89.4%; Score 469.2; DB 3; Length 3434;
Best Local Similarity 97.9%; Pred. No. 2.9e-110;
Matches 507; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
Qy 1 CAAATTTGAGCCAAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 3062 CAAATTTGAGCCAAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 3003
Qy 61 TTTTGACGTTTCTCTAACTACTAAAGGCAATTAATGATCCATAAATATATATCTA 120
Db 3002 TTTTGACGTTTCTCTAACTACTAAAGGCAATTAATGATCCATAAATATATCTA 2943
Qy 121 CATTTACAGCATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180
Db 2942 CATTTACAGCATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 2883
Qy 181 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240
Db 2882 ATTAACAATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 2823
Qy 241 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 300
Db 2822 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 2763
Qy 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 2762 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 2703
Qy 361 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATCTTGAATTCG 420
Db 2702 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATCTTGAATTCG 2643
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Db 2642 ATAGC-AGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATC-AGTATAA 2585

Qy	421	ACAGCAGAGCCTTCTCATCTCTAAACCCCTTCCCTTTTAGTATCTGTGTATCAAGTATAAA	480
Db	2642	ATAGC-AGAGCCTTCTCATCTCTAAACCCCTTCCCTTTTAGTGTCTGTGTATC-AGTATAAA	2585
Qy	481	AGTTCTATAACCTGTAGTNTACTTATTTTAAATCCCCAA	518
Db	2584	AGTTCTATAACCTGTAGT-TACTTATTTTAAATCCCCAA	2548

Search completed: December 31, 2006, 12:31:17
Job time : 125.772 secs

QY 481 AGTTCATAAACTGTAGTACTTATTTAATCCCAA 518
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Db 2584 AGTTCATAAACTGTAGT-TACTTATTTTAATCCCAA 2548
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RESULT 15
US-09-685-166A-476/c
; Sequence 476, Application US/09685166A
; Patent NO. 663035
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-476

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Query Match	89.4%;	Score 469.2;	DB 3;	Length 3434;
Best Local Similarity	97.9%;	Pred. No. 2.9e-110;		
Matches 507;	Conservative 0;	Mismatches 8;	Indels 3;	Gaps 3;
Qy	1	CAAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC	60	
Db	3062	CAAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC	3003	
Qy	61	TTTTGAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATATCTTA	120	
Db	3002	TTTTGAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCATAATAAATACATTATCTA	2943	
Qy	121	CAATTTACAGCATTTAAATATGTGTTTCAGCATGAATATATTAGCTACAGGGGAGCTAAATAA	180	
Db	2942	CAATTTACAGCATTTAAATATGTGTTTCAGCATGAATATATTAGCTACAGGGGAGCTAAATAA	2893	
Qy	181	ATTAACATGGAAATAAGATTTGTGCTTTAAATATAATCTACAAGAAGCTTTTGATATTG	240	
Db	2882	ATTAACATGGAAATAAGATTTGTGCTTTAAATATAATCTACAAGAAGCTTTTGATATTG	2823	
Qy	241	TTTTTCACAAGTGAAGCATTTCTATAAGTGTCATAACCTTTTGGGGAAACTATGGGAA	300	
Db	2822	TTTTTCACAAGTGAAGCATTTCTATAAGTGTCATAACCTTTTGGGGAAACTATGGGAA	2763	
Qy	301	AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTACTCTGAAGCTCAGACTCCATAACC	360	
Db	2762	AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTACTCTGAAGCTCAGACTCCATAACC	2703	
Qy	361	TCTCTTTACAGGAGCTCTCTGCAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTCG	420	
Db	2702	TCTCTTTACAGGAGCTCTCTGCAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTCG	2643	

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 408.854 Seconds
(without alignments)
8969.963 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaatgagcgaatgacat.....tttaatcccaagcacagt 526

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq 8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	3	AA06543 Human imm
2	525	100.0	526	4	AAH93859 Human pro
3	525	100.0	526	4	AA063752 Human pro
4	525	100.0	526	4	AAH02724 Prostate
5	525	100.0	526	4	AAH84973 Human pro
6	525	100.0	526	4	AAH86941 Human P77
7	525	100.0	526	5	ACA59560 Prostate
8	525	100.0	526	6	ABL95123 Human P77
9	525	100.0	526	8	ACC95287 Prostate
10	525	100.0	526	10	ADB13761 Human pro
11	525	100.0	526	10	ADG26177 Human pro
12	525	100.0	526	15	Aef66458 Human pro
13	477.2	90.9	1203	5	ABV27596 Human pro
14	477.2	90.9	1203	5	ABV28357 Human pro
15	477.2	90.9	1203	5	ABV22542 Human pro
16	477.2	90.9	1203	5	ABV21774 Human pro
17	469.2	89.4	634	5	ABV43033 Human pro
18	469.2	89.4	3434	4	AAH93811 Human pro

c 19	469.2	89.4	3434	4	AA063904	AA063904 Human pro
c 20	469.2	89.4	3434	4	AAH85125	AAH85125 Human pro
c 21	469.2	89.4	3434	5	ACA59712	ACA59712 Prostate
c 22	469.2	89.4	3434	6	ABL95275	ABL95275 Human P77
c 23	469.2	89.4	3434	8	ACC95439	ACC95439 Prostate
c 24	469.2	89.4	3434	10	ADB13926	ADB13926 Human pro
c 25	469.2	89.4	3434	10	ADG26342	ADG26342 Human pro
c 26	469.2	89.4	3434	15	AEF66623	AEF66623 Human pro
c 27	387.4	73.8	473	5	ABV13051	ABV13051 Human pro
c 28	372.4	70.9	492	5	ABV34172	ABV34172 Human pro
c 29	330.4	62.9	453	5	ABV03882	ABV03882 Human pro
c 30	265.8	50.6	2413	10	ADB75614	ADB75614 Prostate
c 31	261.6	49.8	2414	4	AAH93810	AAH93810 Human pro
c 32	261.6	49.8	2414	4	AA063903	AA063903 Human pro
c 33	261.6	49.8	2414	4	AAH85124	AAH85124 Human pro
c 34	261.6	49.8	2414	5	ACA59711	ACA59711 Prostate
c 35	261.6	49.8	2414	6	ABL95274	ABL95274 Human P77
c 36	261.6	49.8	2414	8	ACC95438	ACC95438 Prostate
c 37	261.6	49.8	2414	10	ADB13925	ADB13925 Human pro
c 38	261.6	49.8	2414	10	ADG26341	ADG26341 Human pro
c 39	261.6	49.8	2414	15	AEF66622	AEF66622 Human pro
c 40	145.8	27.8	1723	6	AAH38814	AAH38814 Human P77
c 41	109	20.8	1594	4	AAH93809	AAH93809 Human pro
c 42	109	20.8	1594	4	AA063902	AA063902 Human pro
c 43	109	20.8	1594	4	AAH85123	AAH85123 Human pro
c 44	109	20.8	1594	5	ACA59710	ACA59710 Prostate
c 45	109	20.8	1594	6	ABL95273	ABL95273 Human P77

ALIGNMENTS

RESULT 1

AAA06543

ID AAA06543 standard; cDNA; 526 BP.

XX

AC AAA06543;

XX

DT 13-JUN-2000 (first entry)

XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:311.

XX

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

KW immunogenic; cytostatic; vaccine; ss.

XX

OS Homo sapiens.

XX

PN WO200004149-A2.

XX

PD 27-JAN-2000.

XX

PF 14-JUL-1999; 99WO-US015838.

XX

PR 14-JUL-1998; 98US-00115453.

PR

PR 14-JUL-1998; 98US-00116134.

PR

PR 23-SEP-1998; 98US-00159812.

PR

PR 23-SEP-1998; 98US-00159822.

PR

PR 15-JAN-1999; 99US-00232149.

PR

PR 15-JAN-1999; 99US-00232880.

PR

PR 09-APR-1999; 99US-00288946.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;

XX

XX WPI; 2000-171268/15.

XX

PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein.

XX

XX Claim 1; Page 199; 263pp; English.

XX The present invention describes isolated polypeptides, comprising an

CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express the
 CC polypeptides, antibodies against the polypeptides and vaccines comprising
 CC them can be used for inhibiting the development of prostate cancer in a
 CC patient. The polypeptides can be used to generate antibodies or anti-
 CC idotypic antibodies for passive immuno therapy. A portion of the
 CC polynucleotides encoding the polypeptides can be used as a probe or to
 CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
 CC AAY82000 to AAY82020 represent sequences used in the exemplification of
 CC the present invention

XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 3; Length 526;
 Best Local Similarity 100.0%; Pred. No. 4.5e-115;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db |||||||
 Qy 1 CAAATTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
 Db |||||||

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAATTTATATCTA 120
 Db |||||||

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAATTTATATCTA 120
 Db |||||||

Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 180
 Db |||||||

Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 180
 Db |||||||

Qy 181 ATTAACATGGAATGAAGATTGTCCTTAATATAATCTACAAGAGACTTTGATATTG 240
 Db |||||||

Qy 181 ATTAACATGGAATGAAGATTGTCCTTAATATAATCTACAAGAGACTTTGATATTG 240
 Db |||||||

Qy 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300
 Db |||||||

Qy 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300
 Db |||||||

Qy 301 AAAATGGGGAACCTCGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
 Db |||||||

Qy 301 AAAATGGGGAACCTCGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
 Db |||||||

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
 Db |||||||

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
 Db |||||||

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480
 Db |||||||

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480
 Db |||||||

Qy 481 AGTTCTATAAATCTGAGTATGTTTATTTTAAATCCCAAGCAGCAGT 526
 Db |||||||

Qy 481 AGTTCTATAAATCTGAGTATGTTTATTTTAAATCCCAAGCAGCAGT 526
 Db |||||||

RESULT 2

AAH93659

ID AAH93659 standard; cDNA; 526 BP.

XX AC AAH93659;

XX DT 04-OCT-2001 (first entry)

XX DE Human prostate-specific cDNA sequence P775P.

XX DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;

XX KW cytostatic; gene therapy; metastasis; ss.

XX OS Homo sapiens.

XX PN W0200151633-A2.

XX

PD 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;

PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,

PT monitoring and treating prostate cancer in a patient and for use in

PT vaccines.

XX Claim 1; Page 325; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode

CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,

CC and can be used in vaccine production and gene therapy. (I), (II),

CC antibodies to (II), fusion proteins comprising (II), and isolated T cells

CC prepared using (I) or (II) are used treat cancer in a patient. (I) and

CC the antibodies are also used in the detection of cancer in a patient. The

CC cancer that is diagnosed or treated is particularly prostate cancer. (I)

CC and (II) can be used in vaccines. The antibodies or (I) can be used for

CC monitoring the progression of cancer in a patient. (I) and (II) can also

CC be used to improve diagnostic and therapeutic methods for prostate

CC cancer. They can indicate the level of metastasis as well as the prostate

CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent

CC polynucleotide and amino acid sequences used in the exemplification of

CC the present invention

XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Qy Query Match 100.0%; Score 525; DB 4; Length 526;

Db Best Local Similarity 100.0%; Pred. No. 4.5e-115;

Qy Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Db 1 CAAATTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAATTTATATCTA 120

Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAATTTATATCTA 120

Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 180

Db 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATGAAGATTGTCCTTAATATAATCTACAAGAGACTTTGATATTG 240

Db 181 ATTAACATGGAATGAAGATTGTCCTTAATATAATCTACAAGAGACTTTGATATTG 240

Qy 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300

Db 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300

Qy 301 AAAATGGGGAACCTCGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Db 301 AAAATGGGGAACCTCGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480

Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480

QY 481 AGTTCTATAACTGCTAGTNTACTTATTTAATCCCAAGCACAGT 526
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Db 481 AGTTCTATAACTGCTAGTNTACTTATTTAATCCCAAGCACAGT 526

RESULT 3

AAS63752

ID AAS63752 standard; cDNA; 526 BP.

XX AAS63752;

XX 29-JAN-2002 (first entry)

XX Human prostate cDNA sequence #304.

XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009919.

XX 27-MAR-2000; 2000US-00536857.

XX 09-MAY-2000; 2000US-00568100.

XX 12-MAY-2000; 2000US-00570737.

XX 13-JUN-2000; 2000US-00593793.

XX 27-JUN-2000; 2000US-00605783.

XX 09-AUG-2000; 2000US-00636215.

XX 29-AUG-2000; 2000US-00651236.

XX 06-SEP-2000; 2000US-00657279.

XX 02-OCT-2000; 2000US-00679426.

XX 10-OCT-2000; 2000US-00685166.

XX 09-NOV-2000; 2000US-00709729.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

XX Fanger GR, Retter MW, Stolk JH, Day CH, Vedwick TS, Carter D;

XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

XX New human prostate-specific polypeptides and polynucleotides useful for

XX the diagnosis and treatment of cancer, especially prostate cancer.

XX Claim 1; Page 327; 579pp; English.

XX The invention relates to isolated prostate-specific polynucleotides,

XX polypeptides, fusion proteins of the polypeptides, antibodies raised

XX against the polypeptides (or antigenic epitopes derived from them) and

XX antigen-presenting cells expressing the polypeptides. The antibodies are

XX useful for detecting the presence of cancer, especially prostate cancer.

XX The polypeptides, polynucleotides and the antigen-presenting cells are

XX useful for stimulating and/or expanding T cells specific for a tumour

XX protein, and for inhibiting the development of cancer especially prostate

XX cancer. Compositions comprising the polynucleotide and/or polypeptide are

QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATCTA 120
|||||
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATCTA 120
|||||
QY 121 CATTTACAGCATTTAAATGTTTCTAGCATGAATATATTAGCTACAGGGGAAGCTAATAA 180
|||||
Db 121 CATTTACAGCATTTAAATGTTTCTAGCATGAATATATTAGCTACAGGGGAAGCTAATAA 180
|||||
QY 181 ATTAAACATGGAAATAAAGATTGTTCTTAAATATATATCTCAAGAAAGACTTTTGATATTG 240
|||||
Db 181 ATTAAACATGGAAATAAAGATTGTTCTTAAATATATATCTCAAGAAAGACTTTTGATATTG 240
|||||
QY 241 TTTTTCACAAAGTGAAGCAATTTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300
|||||
Db 241 TTTTTCACAAAGTGAAGCAATTTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300
|||||
QY 301 AAAATGGGGAAACTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
|||||
Db 301 AAAATGGGGAAACTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
|||||
QY 361 TCTCTTTACAGGGAGCTCTGCAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
|||||
Db 361 TCTCTTTACAGGGAGCTCTGCAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
|||||
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
|||||
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
|||||
QY 481 AGTTCTATAACTGCTAGTNTACTTATTTAATCCCAAGCACAGT 526
|||||
Db 481 AGTTCTATAACTGCTAGTNTACTTATTTAATCCCAAGCACAGT 526
|||||

RESULT 4

AAH02724

ID AAH02724 standard; cDNA; 526 BP.

XX AAH02724;

XX 14-JUN-2001 (first entry)

XX Prostate tumour antigen determined cDNA sequence for P775P.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;

XX prostate cancer; immunogenic; cytostatic; vaccine; ss.

XX Homo sapiens.

XX WO200125272-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US027464.

XX 04-OCT-1999; 99US-0157455P.

XX (CORI-) CORIXA CORP.

XX Xu J, Skeiky YAW, Reed SG, Cheever MA;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the

XX treatment and diagnosis of prostate cancer.

XX Claim 4; Page 211; 276pp; English.

XX The present invention describes an isolated polypeptide (I) comprising at

XX least an immunogenic portion of a prostate tumour antigen protein or its

XX variant. (I) have cytostatic activity and can be used in vaccine

XX production. (I), prostate tumour antigen polynucleotides, an antigen

XX presenting cell (APC e.g. a dendritic cell) that expresses (I), and a

XX pharmaceutical composition containing (I) are useful for inhibiting the

CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridize to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention
XX

XX SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTAATCTGGGGCCATTTC 60
Db 1 CAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTAATCTGGGGCCATTTC 60
QY 61 TTTTACGCTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
Db 61 TTTTACGCTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
QY 121 CATTTACAGCAATTTAAATGTCTTACAGATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTCTTACAGATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAAGCTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAAGCTTTGATATTG 240
QY 241 TTTTACAGCAATGAGCAATCTTATAAAGTGTCAAACTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTACAGCAATGAGCAATCTTATAAAGTGTCAAACTTTTGGGGAAGCTATGGAA 300
QY 301 AAAATGGGAAACTCTGAGGGTGTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAAACTCTGAGGGTGTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCCTCGAGCCCTTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTCGAGCCCTTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATCTCTGTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATCTCTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526

RESULT 5
AAH84973
ID AAH84973 standard; cDNA; 526 BP.

XX AAH84973;

AC AAH84973;

XX 25-SEP-2001 (first entry)

DE Human prostate-specific cDNA sequence P775P.

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

XX chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX prostate specific antigen; PSA; ss.

XX Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030904.

PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.

XX Claim 5; Page 224-225; 325pp; English.

XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention

XX SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTAATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTAATCTGGGGCCATTTC 60
QY 61 TTTTACGCTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
Db 61 TTTTACGCTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
QY 121 CATTTACAGCAATTTAAATGTCTTACAGATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTCTTACAGATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAAGCTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGAAAGCTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAAACTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAAACTTTTGGGGAAGCTATGGAA 300
QY 301 AAAATGGGAAACTCTGAGGGTGTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAAACTCTGAGGGTGTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCCTCGAGCCCTTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTCGAGCCCTTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATCTCTGTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATCTCTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526

RESULT 6

AAF86941
ID AAF86941 standard; cDNA; 526 BP.
XX
AC AAF86941;
XX
DT 06-JUL-2001 (first entry)
DE Human P775P inventive antigen coding sequence SEQ ID NO: 336.
XX
KW Human; mouse; immunotherapy; cancer; leukaemia; Wt1; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor; ss.
XX
OS Homo sapiens.
XX
PN WO200125273-A2;
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US027465.
XX
PR 04-OCT-1999; 99US-0157459P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX
XX WPI; 2001-328324/34.
XX
PT Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with Wt1.
XX
PS Disclosure; Page 214; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein Wt1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human Wt1
CC proteins are provided. The human Wt1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a coding sequence used in the exemplification of the invention
XX
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATTCTGGGGCCATTTC 60
DB 1 CAAATTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATTCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120
DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120

QY 121 CATTTACAGCAATTTAAATAGTGTTCAGCATGAATAATATTAGCTACAGGGGAAGCTAAATAA 180
DB 121 CATTTACAGCAATTTAAATAGTGTTCAGCATGAATAATATTAGCTACAGGGGAAGCTAAATAA 180

QY 181 ATTAAACATGGAATAAGATTTCTCTCTTAAATATATCTACAGAGAGCTTTTGATATTGG 240
DB 181 ATTAAACATGGAATAAGATTTCTCTCTTAAATATATCTACAGAGAGCTTTTGATATTGG 240

QY 241 TTTTTCACAGTGAAGCAATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
DB 241 TTTTTCACAGTGAAGCAATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300

QY 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

361 TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATAGTGGCTGAGATTCTTGATTGC 420
DB TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATAGTGGCTGAGATTCTTGATTGC 420

QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTATCTGTGTATCAAGTATAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTATCTGTGTATCAAGTATAA 480

QY 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 7
ACA59560
ID ACA59560 standard; cDNA; 526 BP.
XX
AC ACA59560;
XX
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #303.
XX
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR WPI; 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX

PS Example 3; SEQ ID NO 311; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATTATATATCTA 120
Db 61 TTTTGACGTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATTATATATCTA 120

Qy 121 CATTTACAGCATTTAAATGTTTTCAGCATGAAATATTAGCTACAGGGGAGCTTAATAA 180
Db 121 CATTTACAGCATTTAAATGTTTTCAGCATGAAATATTAGCTACAGGGGAGCTTAATAA 180

Qy 181 ATTAACATGGAAATGAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240
Db 181 ATTAACATGGAAATGAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240

Qy 241 TTTTTCACAAGTGAAGCACTTCTTATAAGTGTCATAACCTTTTTCGGGAAACTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCACTTCTTATAAGTGTCATAACCTTTTTCGGGAAACTATGGAA 300

Qy 301 AAAATGGGAAACTCTGAAGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAAC 360
Db 301 AAAATGGGAAACTCTGAAGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAAC 360

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTATGATCTGTGTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTATGATCTGTGTATCAAGTATAAA 480

Qy 481 AGTTCTATAAAGCTAGTNTACTATTTTAAATCCCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTAGTNTACTATTTTAAATCCCCCAAGCACAGT 526

RESULT 8
ID ABL95123
XX ABL95123 standard; cDNA; 526 BP.
XX ABL95123;
XX ABL95123;
DT 19-JUL-2002 (first entry)
XX Human P775P cDNA sequence SEQ ID NO 311.
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX Human; gene therapy; gene; ss.
KW gene therapy; gene; ss.
XX Homo sapiens.

XX US2002022248-A1.
PW 21-FEB-2002.
XX 12-JAN-2001; 2001US-00759143.
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD; Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D; Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
XX Claim 1; SEQ ID NO 311; 87pp; English.
XX The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention
XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATTTGAGCCAAATGACATGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
|||||

PD 02-OCT-2003.

XX 12-NOV-2002; 2002US-002940325.

XX 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 09-FEB-1998; 98US-00020956.

PR 25-FEB-1998; 98US-00030607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00159812.

PR 15-JAN-1999; 99US-00232149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00483672.

PR 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 09-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00685166.

PR 09-NOV-2000; 2000US-00709729.

PR 12-JAN-2001; 2001US-00759143.

PR 09-FEB-2001; 2001US-00780669.

PR 09-MAY-2001; 2001US-00852911.

PR 29-JUN-2001; 2001US-00895814.

PR 10-DEC-2001; 2001US-00012896.

PR 09-MAY-2002; 2002US-00144678.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Kalos MD;

XX WPI; 2003-756193/71.

XX New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.

XX Example 3; Page; 101pp; English.

XX The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB1358, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cut-off value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express the peptides so that the T cells proliferate, and administering the proliferated T cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to

CC stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030195830.

CC Query Match 100.0%; Score 525; DB 10; Length 526;

CC Best Local Similarity 100.0%; Pred. No. 4.5e-115;

CC Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATTAATATATATATCTA 120

Db 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATTAATATATATATCTA 120

Qy 121 CATTTACAGCATTTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

Db 121 CATTTACAGCATTTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATPAAAGATTTTGTCTTAAATATTAATCTACAAGAAGCTTTGATTTG 240

Db 181 ATTAACATGGAATPAAAGATTTTGTCTTAAATATTAATCTACAAGAAGCTTTGATTTG 240

Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACTATGGAA 300

Db 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACTATGGAA 300

Qy 301 AAAATGGGAACTCTCGAAGGTTTAAAGTATCTTACTGAGCTACAGACTCCATAACC 360

Db 301 AAAATGGGAACTCTCGAAGGTTTAAAGTATCTTACTGAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTTGATTGC 420

Db 361 TCTCTTTACAGGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTGTAGTATCTGTATCAAGTATAAA 480

Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTGTAGTATCTGTATCAAGTATAAA 480

Qy 481 AGTTCTATAAACTGTAGTACTTTTAAATCCCAAGCAGT 526

Db 481 AGTTCTATAAACTGTAGTACTTTTAAATCCCAAGCAGT 526

RESULT 11

ADG26177

ID ADG26177 standard; cDNA; 526 BP.

XX AC ADG26177;

XX DT 26-FEB-2004 (first entry)

XX DE Human prostate-specific cDNA #303.

XX Human; prostate-specific polypeptide; gene; ss; prostate cancer; cytostatic.

XX OS Homo sapiens.

XX PN US2003157089-A1.

XX PD 21-AUG-2003.

XX PF 09-MAY-2002; 2002US-00144678.

XX

PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 05-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
 PI Meagher MJ, Deng T;
 XX
 DR WPI; 2003-777973/73.
 XX
 PT New polynucleotides encoding prostate specific polypeptides isolated from
 PT a human prostate tumor cDNA library are useful to diagnose and treat
 PT cancer particularly prostate cancer.
 XX
 PS Example 3; SEQ ID NO 311; 99pp; English.
 XX
 CC The invention relates to human prostate-specific polypeptides and the
 CC polynucleotides encoding them. The invention also relates to an isolated
 CC antibody or its antigen-binding fragment that specifically binds a
 CC polypeptide of the invention, a method of detecting cancer in a patient
 CC comprising contacting a biological sample of the patient with an agent
 CC that binds a prostate-specific polypeptide and comparing the amount of
 CC bound polypeptide compared to a predetermined cut-off value and a fusion
 CC protein comprising a prostate-specific polypeptide. The sequences of the
 CC invention are used to diagnose and treat cancer, particularly prostate
 CC cancer. This sequence represents cDNA encoding a human prostate-specific
 CC polypeptide of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format directly from USPIO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
 Query Match 100.0%; Score 525; DB 10; Length 526;
 Best Local Similarity 100.0%; Pred. No. 4.5e-115;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAATTGAGCCCAATGACATAGAGTTTACAAATCAAGAGCTTATTCTGGGGCCATTTC 60
 DB 1 CAAATTGAGCCCAATGACATAGAGTTTACAAATCAAGAGCTTATTCTGGGGCCATTTC 60
 QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120
 DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120

QY 121 CATTTACAGCATTTAAAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
 DB 121 CATTTACAGCATTTAAAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
 QY 181 ATTAACATGGTAATAAGATTGTCCTTTAAATATAATCTTACAAGAAGACTTTGATATTTC 240
 DB 181 ATTAACATGGTAATAAGATTGTCCTTTAAATATAATCTTACAAGAAGACTTTGATATTTC 240
 QY 241 TTTTTCACAAGTGAAGCACTTCTTATAAAGTGTCTATAAAGCTTTTGGGGAAACTATCGGAA 300
 DB 241 TTTTTCACAAGTGAAGCACTTCTTATAAAGTGTCTATAAAGCTTTTGGGGAAACTATCGGAA 300
 QY 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGCTCCATAACC 360
 DB 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGCTCCATAACC 360
 QY 361 TCTCTTTACAGGAGGCTCTCGAGCCCTACAGAATGAGTGGCTGAGATTCTTGATTGC 420
 DB 361 TCTCTTTACAGGAGGCTCTCGAGCCCTACAGAATGAGTGGCTGAGATTCTTGATTGC 420
 QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAGTATCTGTGTATCAAGTATAA 480
 DB 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAGTATCTGTGTATCAAGTATAA 480
 QY 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGACACAGT 526
 DB 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGACACAGT 526
 RESULT 12
 AEF6458
 ID AEF6458 standard; cDNA; 526 BP.
 XX
 AC AEF66458;
 XX
 DT 06-APR-2006 (first entry)
 XX
 DE Human prostate tumor cDNA clone P775P, SEQ ID 311.
 XX
 KW Cytostatic; Gene Therapy; prostate tumor; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2006024301-A1.
 XX
 PD 02-FEB-2006.
 XX
 PF 23-SEP-2005; 2005US-00234786.
 XX
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW;
 XX
 DR WPI; 2006-117603/12.
 XX
 PT New fusion protein comprising a P501S polypeptide and an unrelated fusion

PT partner, useful for diagnosing, preventing, or treating cancer, such as
PT prostate cancer.
XX
PS Example 3; SEQ ID NO 311; 78pp; English.
XX
XX The present invention relates to prostate-specific fusion proteins and
CC DNA encoding sequences. The fusion proteins can be used for diagnosing,
CC preventing, or treating cancer, such as prostate cancer. The prostate-
CC specific proteins were isolated from a human prostate tumor cDNA library.
CC The present sequence is one such cDNA clone which was isolated in the
CC prostate-specific cDNA library. Note: The sequence data for this patent
CC did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
Query Match 100.0%; Score 525; DB 15; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTATATATCTA 120
Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTATATATCTA 120
QY 121 CATTTACAGCATTTAAATGTTTCCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180
Db 121 CATTTACAGCATTTAAATGTTTCCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCTCTTAAATATATATCTACAAAGAACTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCTCTTAAATATATATCTACAAAGAACTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTCCCAAGCACT 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTCCCAAGCACT 480
QY 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAACTCCCAAGCACT 526
Db 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAACTCCCAAGCACT 526
RESULT 13
ID ABV27596 standard; cDNA; 1203 BP.
XX
AC ABV27596;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27587.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.

XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 5644; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;
Query Match 90.9%; Score 477.2; DB 5; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.2e-103;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
QY 1 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 342 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 401
QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTATATATCTA 120
Db 402 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTATATATCTA 461
QY 121 CATTTACAGCATTTAAATGTTTCCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180
Db 462 CATTTACAGCATTTAAATGTTTCCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 521
QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATATCTACAAAGAACTTTGATATTG 240
Db 522 ATTAACATGGAATAAAGATTGTCTTAAATATATCTACAAAGAACTTTGATATTG 581
QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 582 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 641
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 642 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701
QY 361 TCTCTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 702 TCTCTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 761
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTCTGTATCAAGTATATAA 480

Db 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAGTGTCTGTGTATC-AGTATAAA 819

QY 481 AGTTCTATAAAGCTGTAGTACTTATTTAAATCCCAA 518

Db 820 AGTTCTATAAAGCTGTAGT-TACTTATTTAAATCCCAA 856

RESULT 14

ABV28357

ID ABV28357 standard; cDNA; 1203 BP.

XX AC ABV28357;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 28348.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5909; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;

SQ

Query Match 90.9%; Score 477.2; DB 5; Length 1203;

Best Local Similarity 98.8%; Pred. No. 1.2e-103;

Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 CAAATTTGAGCCAATGACATAGATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60

Db 342 CAAATTTGAGCCAATGACATAGATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 401

QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATTATCTA 120

Db 402 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATTATCTA 461

QY 121 CATTTACAGCATTAAAAATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

Db 462 CATTTACAGCATTAAAAATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 521

QY 181 ATTAACATGGAATAAAGATTGTCTCTTAAATATAATCTACAAGAAGACTTTGATATTTC 240

Db 522 ATTAACATGGAATAAAGATTGTCTCTTAAATATAATCTACAAGAAGACTTTGATATTTC 581

QY 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAACTATGGGAA 300

Db 582 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAAACTATGGGAA 641

QY 301 AAAATGGGAAACTCTGAAGGCTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Db 642 AAAATGGGAAACTCTGAAGGCTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701

QY 361 TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCCTGATTTC 420

Db 702 TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCCTGATTTC 761

QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAACTATCTCTGTATCAAGTATAA 480

Db 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAACTATCTCTGTATCAAGTATAA 819

QY 481 AGTTCTATAAAGCTGTAGTACTTATTTAAATCCCAA 518

Db 820 AGTTCTATAAAGCTGTAGT-TACTTATTTAAATCCCAA 856

RESULT 15

ABV22542

ID ABV22542 standard; cDNA; 1203 BP.

XX AC ABV22542;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 22533.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 3939; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;

Query Match 90.9%; Score 477.2; DB 5; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.2e-103;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 CAATTTTCAGCCCATGACATAGATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db |||||||
QY 342 CAATTTTCAGCCCATGACATAGATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 401
Db |||||||
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAATATATATCTA 120
Db |||||||
QY 402 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAATATATATCTA 461
Db |||||||
QY 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATATTAGCTACAGGGGAAGCTAAATAA 180
Db |||||||
QY 462 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATATTAGCTACAGGGGAAGCTAAATAA 521
Db |||||||
QY 181 ATTTAAACATGGAATAAAGATTTGCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 240
Db |||||||
QY 522 ATTTAAACATGGAATAAAGATTTGCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 581
Db |||||||
QY 241 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
Db |||||||
QY 582 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 641
Db |||||||
QY 301 AAAATGGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 360
Db |||||||
QY 642 AAAATGGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 701
Db |||||||
QY 361 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Db |||||||
QY 702 TCTCTTTACAGGAGCTCTCGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 761
Db |||||||
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATATAA 480
Db |||||||
QY 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTGTCTGTGTATC-AGTATATAA 819
Db |||||||
QY 481 AGTTCTATAAAGTGTAGTACTTATTTTAAATCCCAA 518
Db |||||||
QY 820 AGTTCTATAAAGTGTAGT-TACTTATTTTAAATCCCAA 856
Db |||||||

Search completed: December 31, 2006, 12:54:20
Job time : 409.854 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:13:09 ; Search time 3386.49 Seconds
 (without alignments)
 9932.518 Million cell updates/sec

Title: US-09-232-880-311
 Perfect score: 525
 Sequence: 1 caaatggtgccaatgacat.....ttaaaccacaaagcacagt 526

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
 Total number of hits satisfying chosen parameters: 12732272.

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*
 2: gb_pat.*
 3: gb_ph.*
 4: gb_pl.*
 5: gb_pr.*
 6: gb_ro.*
 7: gb_sts.*
 8: gb_sy.*
 9: gb_un.*
 10: gb_vi.*
 11: gb_ov.*
 12: gb_htg.*
 13: gb_in.*
 14: gb_om.*
 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	2	BD242216 Compounds
2	525	100.0	526	2	AR237399 Sequence
3	525	100.0	526	2	AR278423 Sequence
4	525	100.0	526	2	AR367119 Sequence
5	525	100.0	526	2	AR371015 Sequence
6	525	100.0	526	2	AR400155 Sequence
7	525	100.0	526	2	AR405422 Sequence
8	525	100.0	526	2	AR439626 Sequence
9	525	100.0	526	2	AR563802 Sequence
10	525	100.0	526	2	AR588788 Sequence
11	525	100.0	526	2	AR605608 Sequence
12	525	100.0	526	2	AR656947 Sequence
13	525	100.0	526	2	AR716854 Sequence
14	525	100.0	526	2	AX106198 Sequence
15	525	100.0	526	2	AX106530 Sequence
16	525	100.0	526	2	AX140821 Sequence
17	525	100.0	526	2	AX200681 Sequence
18	525	100.0	526	2	AX267337 Sequence

19	478.8	91.2	154078	5	CNS07BFD
20	478.8	91.2	163976	12	AC080000
21	478.8	91.2	182817	12	AC080181
22	477.2	90.9	1203	2	CQ489898
23	477.2	90.9	1203	2	CQ490668
24	477.2	90.9	1203	2	CQ495743
25	477.2	90.9	1203	2	CQ496503
26	477.2	90.9	161840	5	CNS07BFD
27	474	90.3	176156	5	CNS08CCG
28	470.8	89.7	42301	5	AP000528
29	469.2	89.4	634	2	CQ511185
30	469.2	89.4	876	7	BV572126
31	469.2	89.4	3434	2	AR278575
32	469.2	89.4	3434	2	AR367271
33	469.2	89.4	3434	2	AR400307
34	469.2	89.4	3434	2	AR405574
35	469.2	89.4	3434	2	AR563954
36	469.2	89.4	3434	2	AR588940
37	469.2	89.4	3434	2	AR605760
38	469.2	89.4	3434	2	AR657099
39	469.2	89.4	3434	2	AR717006
40	469.2	89.4	3434	2	AX140986
41	469.2	89.4	3434	2	AX200846
42	469.2	89.4	3434	2	AX267502
43	467.6	89.1	742	7	BV559925
44	467.6	89.1	172816	5	AC123981
45	464.4	88.5	712	7	BV568058

ALIGNMENTS

RESULT 1

BD242216

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD242216 526 bp DNA linear PAT 17-JUL-2003
 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.

BD242216.1 GI:33051986
 JP 2002520054-A/303.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 526)
 Dillon,D.C., Harlocker,S.L., Yuqiu,J., Xu,J. and Mitcham,J.L.
 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use

Patent: JP 2002520054-A 303 09-JUL-2002;

CORIXA CORP

OS Homo sapiens (human)
 PN JP 2002520054-A/303
 PD 09-JUL-2002

PF 14-JUL-1999 JP 2000560247
 PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
 23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
 15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR

PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI
 JIANGCHUN XU,
 JENNIFER LYNN MITCHAM

PC C12N15/09,A61K39/00,A61K39/395,C07K14/47,C07K16/30,
 C12N5/10,
 PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
 PC A61K37/02,
 PC C12N5/00
 CC n = A,T,C or G Location/Qualifiers
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 FT misc feature (1)..(526).
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 /organism="Homo sapiens"

FEATURES

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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGGCAATTAATGATCCATAAATTAATATATCTA 120
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QY 481 AGTTCTATAAAGCTAGTACTTATTTAAATCCCAAGACAGT 526
Db 481 AGTTCTATAAAGCTAGTACTTATTTAAATCCCAAGACAGT 526

RESULT 3
LOCUS AR278423 526 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 311 from patent US 6512094.
ACCESSION AR278423
VERSION AR278423.1 GI:29712669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T., and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 311 28-JAN-2003;
FEATURES Corixa Corporation; Seattle, WA
SOURCE Location/Qualifiers
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Query Match      100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 AGTTCTATAAAGCTAGTACTTATTTAAATCCCAAGACAGT 526
Db 481 AGTTCTATAAAGCTAGTACTTATTTAAATCCCAAGACAGT 526

RESULT 2
LOCUS AR237399 526 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 311 from patent US 6465611.
ACCESSION AR237399
VERSION AR237399.1 GI:27282057
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D. C., and Mitcham, J. L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 311 15-OCT-2002;
FEATURES Corixa Corporation; Seattle, WA
SOURCE Location/Qualifiers
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/organism="unknown"
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Query Match      100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||
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RESULT 6
LOCUS AR400155 526 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 311 from patent US 6620922.
ACCESSION AR400155
VERSION AR400155.1 GI:40143264
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 311 16-SEP-2003;
Corixa Corporation; Seattle, WA
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
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Db |||||||
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RESULT 7
LOCUS AR405422 526 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 311 from patent US 6630305.
ACCESSION AR405422
VERSION AR405422.1 GI:40154259
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 311 07-OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR439626 526 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 311 from patent US 6664377.
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ACCESSION AR439626
VERSION AR439626.1 GI:42665535
KEYWORDS
SOURCE Unknown:
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J.
TITLE Compounds for immunotherapy of prostate cancer and methods for
their use
JOURNAL Patent: US 664377-A 311 16-DEC-2003;
Corixa Corporation; Seattle, WA;
WOX;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
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RESULT 9
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DEFINITION Sequence 311 from patent US 6759515.
ACCESSION AR563802
VERSION AR563802.1 GI:53978853
KEYWORDS
SOURCE Unknown:
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6800746-A 311 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 10
LOCUS AR588788
DEFINITION Sequence 311 from patent US 6800746.
ACCESSION AR588788
VERSION AR588788.1 GI:56635685
KEYWORDS
SOURCE Unknown:
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6800746-A 311 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES
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ORIGIN
Query Match 100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Query Match 100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138; Indels 0; Gaps 0;
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Qy 481 AGTTCTATAAAGCTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
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RESULT 12
LOCUS AR656947 526 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 311 from patent US 6894146.
ACCESSION AR656947
VERSION AR656947.1 GI:67590059
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6894146-A 311 17-MAY-2005;
AUTHORS Corixa Corporation; Seattle, WA
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DEFINITION Sequence 311 from patent US 6818751.
ACCESSION AR605608
VERSION AR605608.1 GI:56657272
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6818751-A 311 16-NOV-2004;
AUTHORS Corixa Corporation; Seattle, WA
FEATURES
source 1..526
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ORIGIN
Query Match 100.0%; Score 525; DB 2; Length 526;
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ACCESSION AR716854
VERSION AR716854.1 GI:77365503
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T., Henderson, R.A., Hural, J., McNeill, P.D., Houghton, R.L.,
Vinals, Y. de Bassols, C., Foy, T.M., Watanabe, Y. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6943236-A 311.13-SEP-2005;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION AX106198
VERSION AX106198.1 GI:13921888
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLE Compositions and methods for wt1 specific immunotherapy
JOURNAL Patent: WO 0125273-A 336.12-APR-2001;
CORIXA CORPORATION (US)
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DEFINITION Sequence 311 from Patent WO0125272.
ACCESSION AX106530
VERSION AX106530.1 GI:13922208
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
AUTHORS Compositions and methods for therapy and diagnosis of prostate
TITLE cancer
JOURNAL Patent: WO 0125272-A 311 12-APR-2001;
FEATURES CORIXA CORPORATION (US)
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Best Local Similarity 100.0%; Pred. No. 2.3e-138; Mismatches 0; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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SUMMARIES

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8	42.4	8.1	2000	10	US-11-299-286-2856
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Sequence 4586, App
Sequence 4, Appl
Sequence 471243,
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Sequence 5907, App

ALIGNMENTS

RESULT 1

US-11-344-932-311

; Sequence 311, Application US/11344932

; Publication No. US20060269532A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Hepler, William T.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals y de Bassols, Carlota

; APPLICANT: Foy, Teresa M.

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Deng, Fa

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C32

; CURRENT APPLICATION NUMBER: 10/11/344,932

; PRIOR FILING DATE: 2006-02-01

; PRIOR APPLICATION NUMBER: 10/144,678

; PRIOR FILING DATE: 2002-05-09

; PRIOR APPLICATION NUMBER: 10/012,896

; PRIOR FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 09/895,814

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 09/852,911

; PRIOR FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: 09/780,669

; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
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; PRIOR FILING DATE: 2000-09-06
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Query Match      100.0%; Score 525; DB 7; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.1e-122; Indels 0; Gaps 0;
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; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
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; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-476
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Query Match      89.4%; Score 469.2; DB 7; Length 3434;
Best Local Similarity 97.9%; Pred. No. 7.4e-108;
Matches 507; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCCTGGGGCCATTTC 60
Db 3062 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCCTGGGGCCATTTC 3003
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATATCTA 120
Db 3002 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 2943
Qy 121 CATTTACAGCAATTTAAATATGTTTCAGCATCAAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 2942 CATTTACAGCAATTTAAATATGTTTCAGCATCAAAATATTAGCTACAGGGGAAGCTAAATAA 2883
Qy 181 ATTAACATGGAATTAAGATTTGTCTTAAATATAATCTACAAAGAGACTTTTGATATTGTG 240
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-344-932-474

Query Match      20.8%; Score 109; DB 7; Length 1594;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 109 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 50

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAT 109
Db 49 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAT 1

RESULT 5
; Sequence 458, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
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; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 458
; LENGTH: 4022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1299, 1372, 1784, 3008, 3018)
; OTHER INFORMATION: unknown base
US-10-517-441-458

Query Match      8.7%; Score 45.8; DB 6; Length 4022;
Best Local Similarity 51.2%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 102;

Qy 69 TTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAAATTTATATTCTACATTTTACA 128
Db 2161 TTTAAATTTTAAAAATAAAATACATAAAAAATAAACTATTACATACGAAAAATACATTAATT 2102

Qy 129 GCATTTAAATGTTCTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAAATAAACA 188
Db 2101 TAATTTAATCTTTAAATAAAAAAACTATTAAAAATTTATCTTTAAATTTAAATTTATAT 2042

Qy 189 TGGATAAAGATTTGCTCTTAAATATAATATCTACAAAGAGACTTTTGATATTTGTTTTTTCAC 248
Db 2041 TAAATTAATAAATTAACCTTTATAAATAATATAATAAATAAATAAATAAATAAATAAATTT 1982

Qy 249 AAGTGAAGCATTTCTTATAAAGTGTCTATAA 277
Db 1981 AAATCAATTTTAAATTAATAATATCATATA 1953

RESULT 6
; Sequence 732, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 732
; LENGTH: 4022
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; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 290
; LENGTH: 16579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-290

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Best Local Similarity 49.3%; Pred. No. 1.4;
Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 19 ATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTCTTTTGACGTTTCTCTAA 78
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Db 1657 ATAGTATTTAAATTAAGATTTTTTTTTTAAATTTTGTGATTTGATTTTTTATAT 1716

QY 79 ACTACTAAAGAGCGATTAATGATCCATAATATATATATCTACATTTACAGCATTTAA 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1717 ATTTGAAATAAGAATTAGATTTTTTTTAAATAAAATTTTAAATTTTATATTTAGAT 1776

QY 139 TGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAATAAATGAATAAAG 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1777 ATTTTGAAGAGTATTTTTTAAGTTAATAATATATATATATATATTTTATTTATAG 1836

QY 199 ATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTGT 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1837 ATTAATTGATAATTTTATAATGAAATAATATATGTTGATAATTTT 1879

RESULT 12
US-10-517-441-564
; Sequence 564, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 564
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; LENGTH: 16579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-564

Query Match      8.0%; Score 42.2; DB 6; Length 16579;
Best Local Similarity 49.3%; Pred. No. 1.4;
Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 19 ATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTCTTTTGACGTTTCTCTAA 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1657 ATAGTATTTAAATTAAGATTTTTTTTTTAAATTTTGTGATTTGATTTTTTATAT 1716

QY 79 ACTACTAAAGAGCGATTAATGATCCATAATATATATATCTACATTTACAGCATTTAA 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1717 ATTTGAAATAAGAATTAGATTTTTTTTAAATAAAATTTTAAATTTTATATTTAGAT 1776

QY 139 TGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAATAAATGAATAAAG 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1777 ATTTTGAAGAGTATTTTTTAAGTTAATAATATATATATATATTTTATTTATAG 1836

QY 199 ATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTGT 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1837 ATTAATTGATAATTTTATAATGAAATAATATATGTTGATAATTTT 1879

RESULT 13
US-10-506-089-9
; Sequence 9, Application US/10506089
; Publication No. US20060234224A1
; GENERAL INFORMATION:
; APPLICANT: Adorjan, Peter
; APPLICANT: Burger, Matthias
; APPLICANT: Maier, Sabine
; APPLICANT: Lesche, Ralf
; APPLICANT: Cottrell, Susan
; APPLICANT: Mooney, Suzanne
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cell prolifer
; TITLE OF INVENTION: disorders
; FILE REFERENCE: 47675-83
; CURRENT APPLICATION NUMBER: US/10/506,089
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/EP03/02034
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: EP 02004551.4
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 110
; SEQ ID NO 9
; LENGTH: 16579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-506-089-9

Query Match      8.0%; Score 42.2; DB 6; Length 16579;
Best Local Similarity 49.3%; Pred. No. 1.4;
Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 19 ATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTCTTTTGACGTTTCTCTAA 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1657 ATAGTATTTAAATTAAGATTTTTTTTTTAAATTTTGTGATTTGATTTTTTATAT 1716

QY 79 ACTACTAAAGAGCGATTAATGATCCATAATATATATCTACATTTACAGCATTTAA 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1717 ATTTGAAATAAGAATTAGATTTTTTTTAAATAAAATTTTAAATTTTATATTTAGAT 1776

QY 139 TGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAATAAATGAATAAAG 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1777 ATTTTGAAGAGTATTTTTTAAGTTAATAATATATATATATATTTTATTTATAG 1836
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:22:01 ; Search time 837.563 Seconds
(without alignments)
7716.790 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaatgagccaatgacat.....tttaatcccaagcacagt 526

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:*

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- 3: /EMC_Celerra_SID83/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SID83/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SID83/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 14: /EMC_Celerra_SID83/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SID83/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SID83/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	3	US-09-759-143-311
2	525	100.0	526	3	US-09-780-669-311
3	525	100.0	526	3	US-09-822-827-311
4	525	100.0	526	3	US-09-232-880-311
5	525	100.0	526	3	US-09-895-793-311
6	525	100.0	526	3	US-09-895-814-311
7	525	100.0	526	6	US-10-012-896-311
8	525	100.0	526	6	US-10-010-940-311
9	525	100.0	526	7	US-10-144-678A-311
10	525	100.0	526	7	US-10-294-025-311
11	525	100.0	526	16	US-11-234-786-311
12	477.2	90.9	1203	9	US-10-357-930-21765
13	477.2	90.9	1203	9	US-10-357-930-22535
14	477.2	90.9	1203	9	US-10-357-930-27610
15	477.2	90.9	1203	9	US-10-357-930-28370
16	469.2	89.4	634	9	US-10-357-930-43052
17	469.2	89.4	3434	3	US-09-759-143-476

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Sequence 476, App	3434	89.4	3434	3	US-09-822-827-476	Sequence 476, App
Sequence 476, App	3434	89.4	3434	3	US-09-895-793-476	Sequence 476, App
Sequence 476, App	3434	89.4	3434	3	US-09-895-814-476	Sequence 476, App
Sequence 476, App	3434	89.4	3434	6	US-10-012-896-476	Sequence 476, App
Sequence 476, App	3434	89.4	3434	6	US-10-010-940-476	Sequence 476, App
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Sequence 13042, A	3434	89.4	3434	16	US-11-234-786-476	Sequence 13042, A
Sequence 34190, A	473	73.8	473	9	US-10-357-930-34190	Sequence 34190, A
Sequence 3873, App	492	70.9	492	9	US-10-357-930-3873	Sequence 3873, App
Sequence 438, App	453	62.9	453	9	US-10-205-823-438	Sequence 438, App
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Sequence 475, App	49.8	2414	49.8	3	US-09-822-827-475	Sequence 475, App
Sequence 475, App	49.8	2414	49.8	3	US-09-895-793-475	Sequence 475, App
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Sequence 475, App	49.8	2414	49.8	6	US-10-012-896-475	Sequence 475, App
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Sequence 475, App	49.8	2414	49.8	7	US-10-144-678A-475	Sequence 475, App
Sequence 475, App	49.8	2414	49.8	7	US-10-294-025-475	Sequence 475, App
Sequence 2, Appli	2414	49.8	2414	16	US-11-234-786-2	Sequence 2, Appli
Sequence 2, Appli	1723	27.8	1723	3	US-09-957-708-2	Sequence 2, Appli
Sequence 474, App	1723	27.8	1723	16	US-11-230-251-2	Sequence 474, App
Sequence 474, App	1594	20.8	1594	3	US-09-759-143-474	Sequence 474, App
Sequence 474, App	1594	20.8	1594	3	US-09-780-669-474	Sequence 474, App

ALIGNMENTS

RESULT 1
US-09-759-143-311

; Sequence 311, Application US/09759143
; Patent No. US2002022248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 311

; LENGTH: 526

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(526)

; OTHER INFORMATION: n = A,T,C or G

; US-09-759-143-311

Query Match 100.0%; Score 525; DB 3; Length 526;

	Best Local Similarity	100.0%; Pred. No.	6.7e-113;	Matches	526; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
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Dd	1	CAAATTTGAGCCAAATGCATAGAATTTTACAANTCAAGAAGCTTATCTCGGGC CATTC	60						
Qy	61	TTTTGACGT TTTTCTTAACCATACTA AAGAGGCAATTAATGATCCATAAATATATATCTA	120						
Dd	61	TTTTGACGT TTTTCTTAACCATACTA AAGAGGCAATTAATGATCCATAAATATATATCTA	120						
Qy	121	CATTTACAGCAATTTAAAAATGTTC CAGCATCAAAATATTAGCTCACAGGGGAAGCTAAATAA	180						
Dd	121	CATTTACAGCAATTTAAAAATGTTC CAGCATCAAAATATTAGCTCACAGGGGAAGCTAAATAA	180						
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Dd	181	ATTAACATGGAATAAAGATTGTCTCTTAATAATAATCTACAAGAAGACTTTTGATTTG	240						
Qy	241	TTTTTTCACAGTGAAGCANCTCTTATAAGTGTGCATACCTTTTGGGGAACCTATGGAA	300						
Dd	241	TTTTTTCACAGTGAAGCANCTCTTATAAGTGTGCATACCTTTTGGGGAACCTATGGAA	300						
Qy	301	AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCCTGAAGCTCACAGCTCCATAACC	360						
Dd	301	AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCCTGAAGCTCACAGCTCCATAACC	360						
Qy	361	TCTCTTTACAGGAGCTCTCGAGCCCCTACAGAAAAGTAGTGGCTGAGATTC TTGATTGC	420						
Dd	361	TCTCTTTACAGGAGCTCTCGAGCCCCTACAGAAAAGTAGTGGCTGAGATTC TTGATTGC	420						
Qy	421	ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTTAGTATCTGTGATCAAGGTATAAA	480						
Dd	421	ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTTAGTATCTGTGATCAAGGTATAAA	480						
Qy	481	AGTTCTATAAAC TGAGTNNTACTTATTTTAAATCCCCAAGCACAGT	526						
Dd	481	AGTTCTATAAAC TGAGTNNTACTTATTTTAAATCCCCAAGCACAGT	526						

RESULT 2

RESUMÉ 2
US-09-780-669-311
; Sequence 311, Application US/09780669
; Patent No. US20020051977A1

; PATENT NO. US2002005
; GENERAL INFORMATION:
; GENERAL INFORMATION:

```

/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqu
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stoik, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ APPLICANT: Hural, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghcon, Raymond L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ DIAGNOSIS OF PROSTATE CANCER
/ FILE OF INVENTION: 210121.427C24
/ FILE REFERENCE: 210121.427C24
/ CURRENT APPLICATION NUMBER: US/09/780,669
/ CURRENT FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 943
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 311

```

```

; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(526)
; OTHER INFORMATION: n = A, T, C or G
US-09-780-669-311

Query Match          100.0%;   Score 525;   DB 3;   Length 526;
Best Local Similarity 100.0%;   Pred. No. 6.7e-113;
Matches 526;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1  CAAATTGGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATTCTCGGGGCCATTTC 60
Db      1  CAAATTTGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATTCTCGGGGCCATTTC 60

Qy      61  TTTTGGAGTTTTCTCTAAAGCTACTAAAGAGGCGATTAATGATCCATAAAATTATATATCTA 120
Db      61  TTTTGGAGTTTTCTCTAAAGCTACTAAAGAGGCGATTAATGATCCATAAAATTATATATCTA 120

Qy      121  CAITTCACAGCATTTAAAAATGTGTTTCAGCATGAATAATTAGCTACAGGGGAAGCTAAATAA 180
Db      121  CAITTCACAGCATTTAAAAATGTGTTTCAGCATGAATAATTAGCTACAGGGGAAGCTAAATAA 180

Qy      181  ATTTAAACATGGAAATAAGAATTTGTCCTTTAAATATAATCTCAAGAAGACCTTTGATATTG 240
Db      181  ATTTAAACATGGAAATAAGAATTTGTCCTTTAAATATAATCTCAAGAAGACCTTTGATATTG 240

Qy      241  TTTTTCACAAGTGAAGCATTCCTTATAAAGTGTCATAACCTTTTGGGGAAAACCTATGGGAA 300
Db      241  TTTTTCACAAGTGAAGCATTCCTTATAAAGTGTCATAACCTTTTGGGGAAAACCTATGGGAA 300

Qy      301  AAAATGGGGAAAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db      301  AAAATGGGGAAAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy      361  TCTCTTTACAGGAGGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
Db      361  TCTCTTTACAGGAGGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420

Qy      421  ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTTTGGTATCTGTGTATCAAGTATAAA 480
Db      421  ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTTTGGTATCTGTGTATCAAGTATAAA 480

Qy      481  AGTTCTATAAACCTGTAGTNTACTATTATTTTAAATCCCCAAAGCACAGT 526
Db      481  AGTTCTATAAACCTGTAGTNTACTATTATTTTAAATCCCCAAAGCACAGT 526

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RESULTS, T 3

```

US-09-822-827-311
; Sequence 311, Application US/09822827
; Patent NO. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-827-311

```

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6,7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTTGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 1 CAAATTTGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATCTGGGGCCATTTC 60
QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120
DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120
QY 121 CATTTACAGCAATTTAAATGTGTTTCAAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
DB 121 CATTTACAGCAATTTAAATGTGTTTCAAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAAACATGGAATAAAGATTGTCCTTAAATATAATCTTACAGAGACTTTGATATTG 240
DB 181 ATTAAACATGGAATAAAGATTGTCCTTAAATATAATCTTACAGAGACTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCAATCTTAAAGTGTCATAACCTTTTGGGGAACTATCGGAA 300
DB 241 TTTTTCACAGTGAAGCAATCTTAAAGTGTCATAACCTTTTGGGGAACTATCGGAA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
DB 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTTGATCAAGTATAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTTGATCAAGTATAA 480
QY 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 4

US-09-232-880-311
; Sequence 311, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-880-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6,7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTTGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 1 CAAATTTGACCAATGACATAGAAATTTTCAAAATCAAGAAGCTTATCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120
DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATATCTA 120
QY 121 CATTTACAGCAATTTAAATGTGTTTCAAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
DB 121 CATTTACAGCAATTTAAATGTGTTTCAAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAAACATGGAATAAAGATTGTCCTTAAATATAATCTTACAGAGACTTTGATATTG 240
DB 181 ATTAAACATGGAATAAAGATTGTCCTTAAATATAATCTTACAGAGACTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCAATCTTAAAGTGTCATAACCTTTTGGGGAACTATCGGAA 300
DB 241 TTTTTCACAGTGAAGCAATCTTAAAGTGTCATAACCTTTTGGGGAACTATCGGAA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
DB 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTTGATCAAGTATAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTTGATCAAGTATAA 480
QY 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAACTGTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 5

US-09-895-793-311
; Sequence 311, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120

Qy 121 CATTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATTAAGATTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240
Db 181 ATTAACATGGAATTAAGATTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240

Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300

Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGAGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480

Qy 481 AGTTCTATAAACTGTAGTNTACTTTTAAATCCCAAGCAGCT 526
Db 481 AGTTCTATAAACTGTAGTNTACTTTTAAATCCCAAGCAGCT 526

RESULT 6
US-09-895-814-311
; Sequence 311, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895.814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120

Qy 121 CATTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATTAAGATTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240
Db 181 ATTAACATGGAATTAAGATTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240

Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300

Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGAGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480

Qy 481 AGTTCTATAAACTGTAGTNTACTTTTAAATCCCAAGCAGCT 526
Db 481 AGTTCTATAAACTGTAGTNTACTTTTAAATCCCAAGCAGCT 526

RESULT 7
US-10-012-896-311
; Sequence 311, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
```


APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 499
OTHER INFORMATION: n = A,T,C or G
US-10-012-896-311

Query Match 100.0%; Score 525; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60
DB 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120
DB 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120
QY 121 CATTTACAGCATTTAAATAGTGTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180
DB 121 CATTTACAGCATTTAAATAGTGTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAGAAGACTTTTGATATTG 240
DB 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATCTACAGAAGACTTTTGATATTG 240
QY 241 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
DB 241 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
QY 301 AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
DB 361 TCTCTTTACAGGAGCTCTCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 8

US-10-010-940-311
Sequence 311, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlock, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or G
US-10-010-940-311

Query Match 100.0%; Score 525; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60
DB 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120
DB 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120
QY 121 CATTTACAGCATTTAAATAGTGTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180
DB 121 CATTTACAGCATTTAAATAGTGTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAGAAGACTTTTGATATTG 240
DB 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATCTACAGAAGACTTTTGATATTG 240
QY 241 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
DB 241 TTTTTCACAAGTGAAGCATCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
QY 301 AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
DB 301 AAAATGGGGAACCTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
DB 361 TCTCTTTACAGGAGCTCTCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526
DB 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 9

US-10-144-678A-311
; Sequence 311, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 499
; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-311

Query Match 100.0%; Score 525; DB 7; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Mismatches 0; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATAATTTAGCTACAGGGAAGCTAAATAA 180
Db 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATAATTTAGCTACAGGGAAGCTAAATAA 180
Qy 181 ATTTAAACATGGAATAAAGATTTGCTCTAAATATAATCTACAAAGAGCTTTGATATTG 240
Db 181 ATTTAAACATGGAATAAAGATTTGCTCTAAATATAATCTACAAAGAGCTTTGATATTG 240
Qy 241 TTTTTCACAGTGAAGCATCTTATTAAGTGTCTAAACCTTTTGGGGAACATATGGAA 300
Db 241 TTTTTCACAGTGAAGCATCTTATTAAGTGTCTAAACCTTTTGGGGAACATATGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGCGTGAGATTTCTTGATTGC 420
Db 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGCGTGAGATTTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTCTAGTATCTGTGTATCAAGATATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTCTAGTATCTGTGTATCAAGATATAA 480
Qy 481 AGTTCTATAAACTGTAGTACTTATTTTAAATCCCAAGACAGT 526
Db 481 AGTTCTATAAACTGTAGTACTTATTTTAAATCCCAAGACAGT 526
RESULT 10
US-10-294-025-311
; Sequence 311, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 499
; OTHER INFORMATION: n = A,T,C or G
US-10-294-025-311

Query Match 100.0%; Score 525; DB 7; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Mismatches 0; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATAATTTAGCTACAGGGAAGCTAAATAA 180
Db 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATAATTTAGCTACAGGGAAGCTAAATAA 180
Qy 181 ATTTAAACATGGAATAAAGATTTGCTCTAAATATAATCTACAAAGAGCTTTGATATTG 240
Db 181 ATTTAAACATGGAATAAAGATTTGCTCTAAATATAATCTACAAAGAGCTTTGATATTG 240
Qy 241 TTTTTCACAGTGAAGCATCTTATTAAGTGTCTAAACCTTTTGGGGAACATATGGAA 300
Db 241 TTTTTCACAGTGAAGCATCTTATTAAGTGTCTAAACCTTTTGGGGAACATATGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGCGTGAGATTTCTTGATTGC 420
Db 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGCGTGAGATTTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTCTAGTATCTGTGTATCAAGATATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTCTAGTATCTGTGTATCAAGATATAA 480

Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTAGTATCTGTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGCAGT 526
Db 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGCAGT 526

RESULT 11

US-11-234-786-311

; Sequence 311, Application US/11234786

; Publication No. US20060024301A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Steiky, Yasir A.

; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION

; FILE REFERENCE: 210121.427C31

; CURRENT APPLICATION NUMBER: US/11/234,786

; CURRENT FILING DATE: 2005-09-23

; PRIOR APPLICATION NUMBER: US 09/568,857

; PRIOR FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: US 09/536,857

; PRIOR FILING DATE: 2000-05-27

; PRIOR APPLICATION NUMBER: US 09/483,672

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: US 09/439,313

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 09/352,616

; PRIOR FILING DATE: 1999-07-13

; PRIOR APPLICATION NUMBER: US 09/288,946

; PRIOR FILING DATE: 1999-04-09

; PRIOR APPLICATION NUMBER: US 09/232,149

; PRIOR FILING DATE: 1999-01-15

; PRIOR APPLICATION NUMBER: US 09/159,812

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: US 09/115,453

; PRIOR FILING DATE: 1998-07-14

; PRIOR APPLICATION NUMBER: US 09/030,607

; PRIOR FILING DATE: 1998-02-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 701

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 311

; LENGTH: 526

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(526)

; OTHER INFORMATION: n = A,T,C or G

US-11-234-786-311

Query Match 100.0%; Score 525; DB 16; Length 526;

Best Local Similarity 100.0%; Pred. No. 6,7e-113;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATTTTGAGCCCAATGACATAGATTTTCAAAATCAAGAGCTTATTTCTGGGGCCATTTC 60

Db 1 CAATTTTGAGCCCAATGACATAGATTTTCAAAATCAAGAGCTTATTTCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCATTAAATGATCCATAAAATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCATTAAATGATCCATAAAATATATCTA 120
QY 121 CATTTACAGCATTTAAATGTGTTGAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCATTTAAATGTGTTGAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
QY 181 ATTAACATGGAATAAAGATTGTCCTTAAATATATCTACAAAGAGACTTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCCTTAAATATATCTACAAAGAGACTTTTGATATTG 240
QY 241 TTTTTCACAAAGTGAAGCATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
Db 241 TTTTTCACAAAGTGAAGCATTTCTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
QY 301 AAAATGGGGAAACTCTGAAAGGGTTTAAAGTATCTTACCTGAAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAACTCTGAAAGGGTTTAAAGTATCTTACCTGAAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCCTGCAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTGCAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAGTATCTGTGTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAGTATCTGTGTATCAAGTATAAA 480
QY 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGCAGT 526
Db 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGCAGT 526

RESULT 12

US-10-357-930-21765

; Sequence 21765, Application US/10357930

; Publication No. US20040259086A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Endegge, Wilson

; APPLICANT: Monahan, John

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

; TITLE OF INVENTION: HUMAN PROSTATE CANCER

; FILE REFERENCE: MRI-007BCN

; CURRENT APPLICATION NUMBER: US/10/357,930

; PRIOR FILING DATE: 2003-02-04

; PRIOR APPLICATION NUMBER: 09/785,276

; PRIOR FILING DATE: 2003-02-16

; PRIOR APPLICATION NUMBER: 60/183,319

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/189,862

; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/207,454

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/211,314

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/219,007

; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 60/255,281

; PRIOR FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 62232

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21765

; LENGTH: 1203

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203

; OTHER INFORMATION: n = A,T,C or G

US-10-357-930-21765

Query Match 90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 CAATTTGAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 342 CAATTTGAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 401
Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
Db 402 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 461
Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTAAGTACAGGGGAAGCTAAATAA 180
Db 462 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTAAGTACAGGGGAAGCTAAATAA 521
Qy 181 ATTAACATGGNAATGAATTTGCTTAAATATAATCTACAGAAGACTTTGATATTTG 240
Db 522 ATTAACATGGNAATGAATTTGCTTAAATATAATCTACAGAAGACTTTGATATTTG 581
Qy 241 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGAA 300
Db 582 TTTTTCACAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGAA 641
Qy 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 642 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701
Qy 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTCG 420
Db 702 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTCG 761
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATC-AGTATAA 819
Qy 481 AGTTCTATAAACTGAGTACTTATTTAATCCCAA 518
Db 820 AGTTCTATAAACTGAGT-TACTTATTTAATCCCAA 856

RESULT 13
US-10-357-930-22535
; Sequence 22535, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 2003-02-04
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22535

LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22535
Query Match 90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 CAATTTGAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 342 CAATTTGAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 401
Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 120
Db 402 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATATCTA 461
Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTAAGTACAGGGGAAGCTAAATAA 180
Db 462 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTAAGTACAGGGGAAGCTAAATAA 521
Qy 181 ATTAACATGGNAATGAATTTGCTTAAATATAATCTACAGAAGACTTTGATATTTG 240
Db 522 ATTAACATGGNAATGAATTTGCTTAAATATAATCTACAGAAGACTTTGATATTTG 581
Qy 241 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGAA 300
Db 582 TTTTTCACAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGAA 641
Qy 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 642 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701
Qy 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTCG 420
Db 702 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTCG 761
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATCAAGTATAAA 480
Db 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGATC-AGTATAA 819
Qy 481 AGTTCTATAAACTGAGTACTTATTTAATCCCAA 518
Db 820 AGTTCTATAAACTGAGT-TACTTATTTAATCCCAA 856

RESULT 14
US-10-357-930-27610
; Sequence 27610, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 2003-02-04
; PRIOR FILING DATE: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:14:13 ; Search time 4216.27 Seconds
(without alignments)
6976.201 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaatgagccaatgacat.....ttaatcccaagcacagt 526

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_ges1:*
12: gb_ges2:*
13: gb_ges3:*
14: gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	361.4	68.8	684	14 AG130449	AG130449 Pan trogl
C 2	335	63.8	678	14 AG093969	AG093969 Pan trogl
C 3	289	55.0	478	11 AQ015128	AQ015128 CIT-HSP-2
C 4	224.2	42.7	597	4 BX098119	BX098119 EX098119
C 5	216.2	41.2	524	1 AA843706	AA843706 aj42f05.s
C 6	178.2	33.9	360	10 R82378	R82378 YJ18b01.r1
C 7	166.8	31.8	301	7 BE694624	BE694624 PMO-BT075
C 8	145.2	27.7	462	1 AA528286	AA528286 nh26d07.s
C 9	144.2	27.5	288	7 BE827798	BE827798 RC2-BT002
C 10	144.2	27.5	554	7 BF001177	BF001177 7g59c10.x
C 11	126.8	24.2	265	1 AA525072	AA525072 nh32h04.s
C 12	124	23.6	559	11 AQ080217	AQ080217 HS 3167 B
C 13	122.4	23.3	577	4 CB049577	CB049577 NISC gj11
C 14	110.6	21.1	434	12 CE393091	CE393091 tigr-gss-
C 15	87	16.6	709	14 AG056621	AG056621 Pan trogl
C 16	60	11.4	298	14 AG201193	AG201193 Pan trogl
C 17	58.2	11.1	432	7 AW971282	AW971282 EST383371
C 18	56.8	10.8	808	11 B2499226	B2499226 BONIL22TF
C 19	56.8	10.8	866	7 BF678216	BF678216 602086120

20 56.8 10.8 997 11 BZ433986
21 55.2 10.5 391 1 AA969621
22 53.4 10.2 1092 14 CNS020K7
23 52 9.9 1101 14 CNS00PMC
24 51 9.7 118 14 AG201107
25 50.8 9.7 710 14 AG368405
26 50.8 9.6 1101 14 CNS016LI
27 50.4 9.6 1043 14 CNS0145P
28 50.2 9.6 971 13 DU092632
29 50.2 9.6 1406 11 BZ563321
30 50 9.5 1101 14 CNS00EVL
31 50 9.5 1272 12 CC264939
32 49.8 9.5 987 14 CNS014PQ
33 49.6 9.4 811 11 BH689045
34 49.6 9.4 1101 14 CNS003BD
35 49.6 9.3 450 9 DN469325
36 48.6 9.3 910 14 AG526131
37 48.4 9.2 1101 14 CNS0039G
38 48 9.1 1101 14 CNS00FVE
39 47.6 9.1 696 13 DU002903
40 47.6 9.1 826 14 DX023921
41 47.6 9.0 501 11 AZ606637
42 47.4 9.0 1165 1 AJ928354
43 47.4 9.0 642 11 AZ606553
44 47.2 9.0 849 14 CR163197
45 47.2 9.0

ALIGNMENTS

RESULT 1
AG130449/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AG130449 684 bp DNA linear GSS 04-NOV-2001
Pan troglodytes DNA, clone: PTB-142D13.F, genomic survey sequence.

AG130449.1 GI:16659614

GSS.

Pan troglodytes (chimpanzee)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 684)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan (E-mail: chimpes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. 684

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="PTB-142D13.F"

/sex="male"

source	1. .678	/organism="Pan troglodytes"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9598"	
		/clone="PTB-094J13.F"	
		/sex="male"	
		/cell_type="lymphoblast"	
		/clone_lib="PTB Chimpanzee Male BAC Library"	
ORIGIN			
Query Match	63.8%;	Score 335;	DB 14; Length 678;
Best Local Similarity	94.5%;	Pred. No. 9.8e-68;	
Matches 358;	Conservative	0; Mismatches 20;	Indels 1; Gaps 1
Qy	1	CAAAATTGGAGCCAAATGACATAGAAATTTTACAATCAAGAAGCTTATCTCTGGGGCCATTTC	60
Db	456	CAAAATTGATCCAAATGACATAGAAATTTTACAATCAAGAAGCTTATCTCTGGGGCCAGTTC	397
Qy	61	TTTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATTATCTA	120
Db	396	TTTGACGTTTCTCTGTAACACTAAAGAGGCAATTAATGATCCATAAAATATATATTATCTA	337
Qy	121	CATTACAGCAATTTAAATGTGTTACAGCATGAATAATTAGCTACAGGGAAGCTTAAATAA	180
Db	336	CATTACAGCAATTTAAATGTGTTACAGCATGAATAATTAGCTACAGTGAAGCTTAAATAA	277
Qy	181	ATTAAACATGGATAAAGATTCTGCTTAAATATATCTACAAGAAGACTTTTGATATTTG	240
Db	276	ATTAAACATGGATAAAGATTCTGCTTAAATATATCTACAAGAAGACTTTTGATATTTG	217
Qy	241	TTTTTCCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTTGGGGAACATATGGAA	300
Db	216	TTTTTCCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTTGGGGAACATATGGAA	157
Qy	301	AAATGGGGAACCTCGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC	360
Db	156	AAATGGGGAACCTCGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC	97
Qy	361	TCCTCTTTACAGGAGCTCC	379
Db	96	TCCTCTTTACAGGAGCTCC	78
RESULT 2			
AG093969/c			
LOCUS	AG093969	678 bp	DNA linear GSS 03-NOV-2001
DEFINITION	Pan troglodytes DNA, clone: PTB-094J13.F, genomic survey sequence.		
ACCESSION	AG093969		
VERSION	AG093969.1	GI:16645771	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE			
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.		
TITLE	BAC end sequences of Library PTB		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
COMMENT	Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.		
PRIMERS			
Sequencing:	-21M13		
LIBRARY			
Vector	: pKS145		
R.Site 1	: SacI		
R.Site 2	: SacI.		
Location/Qualifiers			
FEATURES			

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1..478
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2301D2"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 55.0%; Score 289; DB 11; Length 478;
Best Local Similarity 93.8%; Pred. No. 5.6e-57;
Matches 323; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
QY 1 CAAATTGAGCCAATCACATAGAAATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 410 CATACTTGAGTCAGTCAAGCAATGGAATTTTACAACCAAGAAGCTTATCTAGGGCCATTTC 351
QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAAATTATATTATCTA 120
DB 350 TTTTGAAGTTTCTTAACACTACTAAAGAGACATTAATGATCCATAAAATTACATTATCTA 291
QY 121 CATTTCACAGATTAAATGTGTTACAGATGAATATTAGCTACAGGGAAGCTAAATAA 180
DB 290 CATTTCACAGATTAAATGTGTTACAGATGAATATTAGCTACAGGGAAGCTAAATAA 231
QY 181 ATTAACATGGTAATGAATGTTCTCTTAATATATCTACAGAGACTTTTGATATTG 240
DB 230 ATAAACATGGTAATGAATGTTCTCTTAATATGATTTTACAAGAAGA-TTTTATATTG 172
QY 241 TTTTTCACAGTGAAGCAATCTTATAAGGTGTCATAACCTTTTGGGGAAACTATGGGAA 300
DB 171 TTTTTCACAGTGAAGCAATCTTATAAGGTGTCATAACCTTTTGGGGAAACTCTGGG-A 113
QY 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCT 345
DB 112 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTCTGAAGCT 68

RESULT 4

BX098119/c
LOCUS BX098119 Soares placenta Nb2HP Homo sapiens cDNA clone
DEFINITION IMAGp998102228 ; IMAGE:149065, mRNA sequence.
ACCESSION BX098119 GI:27829237
VERSION BX098119.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 597)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998102228.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCCACAGAAACAGCTATGAC.

FEATURES

Location/Qualifiers
1..597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998102228 ; IMAGE:149065"
/sex="Female"
/lab_host="DH10B (ampicillin resistant)"
/dev stages="placenta obtained at birth (full term)"
/clone_lib="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: p7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGAATTCGCCGCCGAGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match 42.7%; Score 224.2; DB 4; Length 597;
Best Local Similarity 97.9%; Pred. No. 8.6e-42;
Matches 238; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 241 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCC--ATT 184
QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGCAATTAATGATCCATAAAATTATATTATCTA 120
DB 183 CTTTGACGTTTCTCTAAACTACTAAAGAGCAATTAATGATCCATAAAATTATATTATCTA 124
QY 121 CATTTCACAGCATTTAAATGTGTTACAGATGAATATTAGCTACAGGGAAGCTAAATAA 180
DB 123 CATTTCACAGCATTTAAATGTGTTACAGATGAATATTAGCTACAGGGAAGCTAAATAA 64
QY 181 ATTAACATGGTAATGAATGTTCTCTTAATATATATCTACAAGAAGACTTTGATATTG 240
DB 63 ATTAACATGGTAATGAATGTTCTCTTAATATATATCTACAAGAAGACTTTGATATTG 4
QY 241 TTT 243
DB 3 TTT 1

RESULT 5

AA843706
LOCUS AA843706 524 bp mRNA linear EST 31-DEC-1998
DEFINITION aj42f05.sl Soares testis_NHT Homo sapiens cDNA clone IMAGE:1392993
ACCESSION AA843706
VERSION AA843706.1 GI:2933062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 948 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 474.
 Location/Qualifiers

FEATURES

source

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1..524
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1392993"
/sex="male"
/lab host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT73D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was prepared from mRNA obtained from
Clontech Laboratories, Inc., and primed with a Not I -
oligo(dT) primer [5',
TGTACCAATCTGAATCGGAGCGGCCCAATTTTTTTTTTTT 3']."
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
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ORIGIN

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Query Match      41.2%; Score 216.2; DB 1; Length 524;
Best Local Similarity 98.6%; Pred. No. 6.3e-40;
Matches 218; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
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Db 304 CAAATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 363

QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 120
   |||||
Db 364 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATCTA 423

QY 121 CATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 180
   |||||
Db 424 CATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 483

QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTAC 221
   |||||
Db 484 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTAC 524
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RESULT 6
R82378/c
LOCUS      R82378      360 bp      mRNA      linear      EST 14-JUN-1995
DEFINITION YJ18b01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:149065 5', mRNA sequence.
ACCESSION R82378
VERSION    R82378.1 GI:861769
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 360)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Meara, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
```

```

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
```

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 694
 High quality sequence stops: 238
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 694 Std Error: 0.00
 Seg primer: M13RP1
 High quality sequence stop: 238.
 Location/Qualifiers

FEATURES

source

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1..360
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/mol_type="mRNA"
/db_xref="GDB:560899"
/db_xref="taxon:9606"
/clone="IMAGE:149065"
/sex="Female"
/dev stage="placenta obtained at birth (full term)"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/notes="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AATCGGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

```

Query Match      33.9%; Score 178.2; DB 10; Length 360;
Best Local Similarity 95.1%; Pred. No. 4.8e-31;
Matches 195; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 2 AAAATTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 61
   |||||
Db 203 AATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGC--ATTTC 146

QY 62 TTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTAC 121
   |||||
Db 145 TTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTAC 86

QY 122 ATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 181
   |||||
Db 85 ATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGTACAGGGGAAGCTAAATAA 26

QY 182 TTAACATGGAATAAAGATTGTGTC 206
   |||||
Db 25 TTAACATGGAATAAAGATTGTGTC 1
```

RESULT 7

BE694624

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 301)

Dias Neto, E., Garcia

Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t=PMO-BT0757-240
500-003-D01&t3=2000-05-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 301.

FEATURES
source

ORIGIN

Query Match	31.8%	Score 166.8;	DB 7;	Length 301;
Best Local Similarity	93.2%;	Pred. No. 2.2e-28;		
Matches 207;	Conservative 0;	Mismatches 12;	Indels 3;	Gaps 3;
QY	297	GGAAAAATCGGGGAAACTCTGGAAGGGTTTTAAAGTATCTTACCTGAAAGCTACAGACTCCAT	356	
Db	5	GGAGAAATGGAGAAACTCTGAAGGGTTTTTAAGTACCTTTCTGGAAGCTCGAGCTCCAT	64	
QY	357	AACCTCTCTTTACAGGGAGCTCTCGCAGCCCTACAGAAATGATGGCTGAGATCTTTGA	416	
Db	65	AACCTCTCTTTACAAAGAGCTCTCGCAGCTCTCTACAGAAATGATGGCTGAGATCTTTGA	124	
QY	417	TTGCAGCAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTACTACTCTGTGTATCAAGTA	476	
Db	125	TTGCATAGC-AGAGCTTCTCATCAAAACCCTTTCCCTTTTGTGTCTGTGTATC-AGTA	182	
QY	477	TAAAGTTCATAAACTGTAGTACTTATTTTAAATCCCCAA	518	
Db	183	TAAAGTTCATAAACTGTAGT-TACTATTTTAAATCCCCAA	223	

RESULT	8
AA528286/c	
LOCUS	
DEFINITION	AA528286 462 bp mRNA linear EST 05-AUG-1997 nh26d07.s1 NCI_CGAP_Pr-3 Homo sapiens cDNA clone IMAGE:553485, mRNA sequence.
ACCESSION	AA528286
VERSION	AA528286.1 GI:2270355
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 462) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE	

**JOURNAL
COMMENT**

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 890 Std Error: 0.00
Seq primer: ~40ml3 fwd. ET from Amersham
High quality sequence stop: 325.

FEATURES
source

ORIGIN

	Query Match	27.7%;	Score 145.2;	DB 1;	Length 462;
	Best Local Similarity	91.6%;	Pred. No. 2.6e-23;		
Matches	175; Conservative	0; Mismatches	14; Indels	2; Gaps	2;
QY	328 AGTATCTTAACCTGAAGCTACAGACTCATAA	CCTCTCTTTACAGGGAGGCTCCTGCAGCCC	387		
Db	434 AGTGGTTCCTTGAGCTACAGATCCATA	A CCTCTCTTTAGAGGAGGTCTCTGCAGCCC	375		
QY	388 CTACAGAAATGATGGCTGAGATTCTTGATTG	CACAGCAAGAGCTTCTCATCTAAACCCT	447		
Db	374 ATACAGAAATGATGGCTGAGATTCTTGATTG	CATAGC-AGAGCTTCTCATCTAAACCCT	316		
QY	448 TTCCCTTTTTTAGTATCTGTGTATCAAGTATA	AAAAGTTCTATAAACCTGTAGTACTATT	507		
Db	315 TTCCCTTTTTTAGTGTCTGTATC-AGTATA	AAAAGTTCTATAAACCTGTAGTACTATT	257		
QY	508 TTAATCCCCAA	518			
Db	256 TTAATCCCCAA	246			

RESULT 9

BE827798	288 bp	linear	EST 22-SEP-2000
LOCUS			
DEFINITION	RC2-EU0022-170500-015-all EU0022 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BE827798		
VERSION	BE827798.1		
KEYWORDS	GI:10260176		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 288)		

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC2-ET0022-170500-015-all&t3=2000-05-17&t4=1)
500-015-all&t3=2000-05-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 288.

FEATURES source
1..288
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0022"
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 27.5%; Score 144.2; DB 7; Length 288;
Best Local Similarity 96.8%; Pred. No. 4.3e-23;
Matches 179; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 334 TTACCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCCTGCAGGCCCTACAG 393
Db 88 TTACCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCCTGCAGGCCCTACAG 147
Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGAGAGCTTCTCATCTAAACCCCTTCCCT 453
Db 148 AAATGAGTGGCTGAGATCTTGATTGCACAGC-AGAGCTTCTCATCTAAACCCCTTCCCT 206
Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAGTCTATATAAGTCTAGTNTACTTTTAAATC 513
Db 207 TTTTAGTGTGTGTATC-AGTATAAAGTTCTATAAAGTCTAGT-TACTTATTTTAAATC 264
Qy 514 CCAAA 518
Db 265 CCAAA 269

RESULT 10
BF001177
LOCUS BF001177
DEFINITION BF001177 554 bp mRNA linear EST 06-OCT-2000
7959c10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3310770 3', mRNA sequence.
ACCESSION BF001177
VERSION BF001177.1 GI:10701452
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 554)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapsb-femail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. consortium/LINL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 432.

FEATURES source
1..554
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3310770"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (Clones 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 27.5%; Score 144.2; DB 7; Length 554;
Best Local Similarity 96.8%; Pred. No. 4.6e-23;
Matches 179; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 334 TTACCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCCTGCAGGCCCTACAG 393
Db 325 TTACCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCCTGCAGGCCCTACAG 384
Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGAGAGCTTCTCATCTAAACCCCTTCCCT 453
Db 385 AAATGAGTGGCTGAGATCTTGATTGCATAGC-AGAGCTTCTCATCTAAACCCCTTCCCT 443
Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAAGTTCTATAAAGTCTAGTNTACTTTTAAATC 513
Db 444 TTTTAGTGTGTGTATC-AGTATAAAGTTCTATAAAGTCTAGT-TACTTATTTTAAATC 501
Qy 514 CCAAA 518
Db 502 CCAAA 506

RESULT 11
AA525072/c
LOCUS AA525072
DEFINITION nh32h04.b1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:954103, mRNA sequence.
ACCESSION AA525072
VERSION AA525072.1 GI:2266000
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

REFERENCE
 1 (bases 1 to 265)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,
 M.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. RT from Amersham.

FEATURES

Location/Qualifiers
 1..265
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:954103"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr3"
 /note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from
 5,000-10,000 microdissected cells
 histologically-determined to be fully malignant prostate
 cancer cells. Double-stranded cDNA was ligated to EcoRI
 adaptors, 5 cycles of PCR applied to the cDNA with an
 adaptor-specific primer, and the resulting PCR product
 subcloned into pAMP10 by the UDG-cloning method (life
 technologies). Average insert size is 600 bp. NOTE: Not
 directionally cloned. This library was constructed by
 David Krizman."

ORIGIN

Query Match 24.2%; Score 126.8; DB 1; Length 265;
 Best Local Similarity 97.9%; Pred. No. 5e-19;
 Matches 139; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 334 TTACCTGAAGCTACAGACTCCATAAAGCTCTTTACAGGAGCTCTCTGAGCCCTACAG 393
 DB 146 TTACCTGAAGCTACAGACTCCATAAAGCTCTTTACAGGAGCTCTCTGAGCCCTACAG 87
 QY 394 AAATGAGTGGCTGAGATTCTTGATTCACAGCAAGAGCTTCTCATCTAAACCCCTTCCCT 453
 DB 86 AAATGAGTGGCTGAGATTCTTGATTCACAGCAAGAGCTTCTCATCTAAACCCCTTCCCT 28
 QY 454 TTTTAGTATCTGTGTATCAAGT 475
 DB 27 TTTTAGTATCTGTGTATCAAGT 6

RESULT 12
 AQ802217/c
 LOCUS
 DEFINITION
 HS_3167_B2_D11_T7C CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3167 Col=22 Row=H, genomic survey
 sequence.
 ACCESSION
 AQ802217
 VERSION
 AQ802217.1 GI:5719549
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 559)

AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT

Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 3167 row: H Column: 22
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 559.

FEATURES

Location/Qualifiers
 1..559
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3167 Col=22 Row=H"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
 E-Coli DH10B"

ORIGIN

Query Match 23.6%; Score 124; DB 11; Length 559;
 Best Local Similarity 91.1%; Pred. No. 2.5e-18;
 Matches 163; Conservative 0; Mismatches 13; Indels 3; Gaps 3;
 QY 337 CCTGAAGCTACAGACTCCATAAAGCTCTTTACAGGAGCTCTCTGAGCCCTACAGAAA 396
 DB 553 CCTGAAGATGCAGACTCCATACCTCTTTACANAGAGCTCTGAGCTCATACAGAGA 494
 QY 397 TGAGTGGCTGAGATTCTTGATTCACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTT 456
 DB 493 TGAGTGGCTGAGATTCTTGATTCAGCATAGC-AGAGCTTCTCATCTAAACCCCTTCCCTTTT 435
 QY 457 TAGTATCTGTGTATCAAGTATATAAGTCTCTATAAACTAGTNTACTTTTAAATCCC 515
 DB 434 TAGTGTCTGTGTATC-AGTATAAAGTCTCTATAAACTGTAGT-TACTTATTTTAAATCCC 378

RESULT 13

CB049577
 LOCUS
 DEFINITION
 NISC G111g01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271488
 3', mRNA sequence.
 ACCESSION
 CB049577
 VERSION
 CB049577.1 GI:27787864
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 577)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 CDNA Library Preparation:
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)

Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Plate: L1AM8008 row: N column: 1
 Seq primer: -21M13 forward primer (ABI).

FEATURES

source
 1. .577
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="IMAGE:3271488"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CCAP Pr28"
 /note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA from the normalized library NCI CCAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 23.3%; Score 122.4; DB 4; Length 577;
 Best Local Similarity 89.7%; Pred. No. 5.9e-18;
 Matches 165; Conservative 0; Mismatches 16; Indels 3; Gaps 3;
 Qy 334 TTACTGAGCTACAGCTCCTACCTCTCTTTACAGGGAGCTCTCGACGCCCTACAG 393
 Db 397 TTACTGAACTACAACTCCATACCTTTTTTTACAGGGAGCTCTCGACGCCCTACAA 456
 Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGCAGCTTCTCATCTAAACCTTTCCCT 453
 Db 457 AAATGAGTGGCTGAAATTTTGAATTCACAAACA- AACTTTTCATCTAAACCTTTCCCT 515
 Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAAGTTCTCTATAAAGCTGTAGTACTTTTAAATC 513
 Db 516 TTTTAGGGCTGGGTATCAAA-AATAAAGTTCTATAAAGCTGTAGT-TACTTTTAAATC 573
 Qy 514 CCCA 517
 Db 574 CCAA 577

RESULT 14

CE393091/c
 LOCUS
 DEFINITION
 tigr-gss-dog-17000334478329 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION

CE393091

VERSION

CE393091.1 GI:36634243

KEYWORDS

GSS.

SOURCE

Canis familiaris (dog)

ORGANISM

Canis familiaris

REFERENCE

1 (bases 1 to 434)
 Kirckness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 14512627

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

FEATURES

source
 1. .434
 Location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 21.1%; Score 110.6; DB 12; Length 434;
 Best Local Similarity 73.1%; Pred. No. 3.3e-15;
 Matches 185; Conservative 0; Mismatches 59; Indels 9; Gaps 3;
 Qy 1 CAAATTTGAGCCAATGACATAGAAATTTTACAA-ATCAAGAAGCTTTATCTGGGCCCATTT 59
 Db 253 CAACTTGAGTTAATGGCAGAGATTTTACAAGATCAAAAAGCTTTCATCTAGAGCCATTT 194
 Qy 60 CTTTGTGACGTTTCTCTAAACTACTAAAGAGGC-ATTAAATGATCCATAAATATATATATC 118
 Db 193 CTTTTTAAGTTCTTCTTAAGCTACTCAAGAGGCAACTGGTTCTCCATAAATATATATATC 134
 Qy 119 TACATTTTACAGCATT-----TAAATGTGTCAGCATGAATATAGCTACAGGGGAA 171
 Db 133 TACCTTTTACAGGATTAATAAAAAAATGTGTGGGATGCAACATTAGCTCTAGTGTTA 74
 Qy 172 GCTAAATAAATTAACATGGAATAAGATTTGTCTTAAATATAATCTTACAAGAAGACTT 231
 Db 73 GCTAAGTAAATTAACAGGGAATAAGCTTTGAICTTAAATAATCATTACCAGAAGATCT 14
 Qy 232 TGATATTTGTTTT 244
 Db 13 TAATATTTGTTTT 1

RESULT 15

AG056621
 LOCUS

DEFINITION

Pan troglodytes DNA, clone: PTB-042P10.F, genomic survey sequence.

ACCESSION

AG056621

VERSION

AG056621.1 GI:16594080

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

REFERENCE

1

AUTHORS

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE

BAC end sequences of Library PTB

JOURNAL

Unpublished

AUTHORS

2 (bases 1 to 709)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.

FEATURES

source Location/Qualifiers
1. .709
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-042P10.P"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 16.6%; Score 87; DB 14; Length 709;
Best Local Similarity 78.8%; Pred. No. 1.2e-09;
Matches 141; Conservative 0; Mismatches 35; Indels 3; Gaps 3;
QY 340 GAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCTGCAGCCCTACAGAAATGA 399
|||
Db 64 GATCATACGGCTTCGAAAGCTTCGCGACGTACGACGTCGCGGAGCTCTGCAGAAATGA 123
QY 400 GTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAG 459
|||
Db 124 GTGGCTGAGATTCTGTGTCATAGC-AGAGCTTCTCATCCAAACCCTTTCCCTTTTAG 182
QY 460 TATCTGTGTATCAAGTATAAAAGTTCTATAAACTAGTAGTACTTATTTTAAATCCCAA 518
|||
Db 183 TGTCTGTGTATC-AGTATAAAGTTCTATAAACAGTAGT-TACTTATTTTAAATCCCAA 239

Search completed: December 31, 2006, 19:30:59
Job time : 4220.27 secs

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